FIG.1A

Human Glial Cell Line-Derived
Neurotrophic Factor Receptor Protein

```
         10                  30                  50
AATCTGGCCTCGGAACACGCCATTCTCCGCGCCGCTTCCAATAACCACTAACATCCCTA

         70                  90                 110
ACGAGCATCCGAGCCGAGGGCTCTGCTCGGAAATCGTCCTGGCCCAACTCGGCCCTTCGA

        130                 150                 170
GCTCTCGAAGATTACCGCATCTATTTTTTTTTTCTTTTTTTTCTTTTCCTAGCGCAGATA
```

FIG.1B

190 210 230
AAGTGAGCCCGGAAAGGGAAGGAGGGGGCGGGACACCATTGCCCTGAAAGAATAAATAA

250 270 290
GTAAATAAACAAACTGGCTCCTCGCCGCAGCTGGACGCGGTCGGTTGAGTCCAGGTTGGG

310 330 350
TCGGACCTGAACCCCTAAAAGCGGAACCGCCTCCCGCCCTCGCCATCCCGGAGCTGAGTC

370 390 410
GCCGGCGGCGGTGGCTGCTGCCAGACCCGGAGTTTCCTCTTTCACTGGATGGAGCTGAAC

FIG.1C

```
           430                 450                 470
TTTGGGCGGCCAGAGCAGCACAGCTGTCCGGGGATCGCTGCACGCTGAGCTCCCTCGGCA

           490                 510                 530
AGACCCAGCGGCGGCTCGGGATTTTTTGGGGGGCGGGGACCAGCCCCGCGCCGGCACC

           550                 570                 590
ATGTTCCTGGCGACCCTGTACTTCGCGCTGCCGCTCTTGGACTTGCTCCTGTCGGCCGAA
M  F  L  A  T  L  Y  F  A  L  P  L  L  D  L  L  L  S  A  E
```

FIG.1D

```
          610                 630                 650
GTGAGCGGCGGAGACCGCCTGGATTGCGTGAAAGCCAGTGATCAGTGCCTGAAGGAGCAG
V  S  G  G  D  R  L  D  C  V  K  A  S  D  Q  C  L  K  E  Q

          670                 690                 710
AGCTGCAGCACCAAGTACCGCACGCTAAGGCAGTGCGTGGCGGGCAAGGAGACCAACTTC
S  C  S  T  K  Y  R  T  L  R  Q  C  V  A  G  K  E  T  N  F

          730                 750                 770
AGCCTGGCATCCGGCCTGGAGGCCAAGGATGAGTGCCGCAGCGCCATGGAGGCCCTGAAG
S  L  A  S  G  L  E  A  K  D  E  C  R  S  A  M  E  A  L  K
```

FIG.1E

```
             790                           810                           830
CAGAAGTCGCTCTACAACTGCCGCTGCAAGCGGGGTATGAAGAAGGAGAAGAACTGCCTG
Q  K  S  L  Y  N  C  R  C  K  R  G  M  K  K  E  K  N  C  L

             850                           870                           890
CGCATTTACTGGAGCATGTACCAGAGCCTGCAGGGAAATGATCTGCTGGAGGATTCCCCA
R  I  Y  W  S  M  Y  Q  S  L  Q  G  N  D  L  L  E  D  S  P

             910                           930                           950
TATGAACCAGTTAACAGCAGATTGTCAGATATATTCCGGGTGGTCCCATTCATATCAGAT
Y  E  P  V  N  S  R  L  S  D  I  F  R  V  V  P  F  I  S  D
```

FIG.1F

```
          970                 990                 1010
GTTTTTCAGCAAGTGGAGCACATTCCCAAAGGGAACAACTGCCTGGATGCAGCGAAGGCC
V  F  Q  Q  V  E  H  I  P  K  G  N  N  C  L  D  A  A  K  A

         1030                1050                1070
TGCAACCTCGACGACATTTGCAAGAAGTACAGGTCGGCGTACATCACCCCGTGCACCACC
C  N  L  D  D  I  C  K  K  Y  R  S  A  Y  I  T  P  C  T  T

         1090                1110                1130
AGCGTGTCCAACGATGTCTGCAACCGCCGCAAGTGCCACAAGGCCCTCCGGCAGTTCTTT
S  V  S  N  D  V  C  N  R  R  K  C  H  K  A  L  R  Q  F  F
```

FIG.1G

```
         1150                1170                1190
GACAAGGTCCCGGCCAAGCACAGCTACGGAATGCTCTTCTGCTCCTGCCGGGACATCGCC
D  K  V  P  A  K  H  S  Y  G  M  L  F  C  S  C  R  D  I  A

         1210                1230                1250
TGCACAGAGCGGAGGCGACAGACCATCGTGCCTGTGTGCTCCTATGAAGAGAGGGAGAAG
C  T  E  R  R  R  Q  T  I  V  P  V  C  S  Y  E  E  R  E  K

         1270                1290                1310
CCCAACTGTTTGAATTTGCAGGACTCCTGCAAGACGAATTACATCTGCAGATCTCGCCTT
P  N  C  L  N  L  Q  D  S  C  K  T  N  Y  I  C  R  S  R  L
```

FIG.1H

```
        1330                1350                1370
GCGGATTTTTTACCAACTGCCAGCCAGAGTCAAGGTCTGTCAGCAGCTGTCTAAAGGAA
A  D  F  F  T  N  C  Q  P  E  S  R  S  V  S  S  C  L  K  E

        1390                1410                1430
AACTACGCTGACTGCCTCCTCGCCTACTCGGGGCTTATTGGCACAGTCATGACCCCCAAC
N  Y  A  D  C  L  L  A  Y  S  G  L  I  G  T  V  M  T  P  N

        1450                1470                1490
TACATAGACTCCAGTAGCCTCAGTGTGGCCCCATGGTGTGACTGCAGCAACAGTGGGAAC
Y  I  D  S  S  S  L  S  V  A  P  W  C  D  C  S  N  S  G  N
```

FIG.1I

```
        1510                1530                1550
GACCTAGAAGAGTGCTTGAAATTTTTGAATTTCTTCAAGGACAATACATGTCTTAAAAAT
D  L  E  E  C  L  K  F  L  N  F  F  K  D  N  T  C  L  K  N

        1570                1590                1610
GCAATTCAAGCCTTTGGCAATGGCTCCGATGTGACCGTGTGGCAGCCAGCCTTCCCAGTA
A  I  Q  A  F  G  N  G  S  D  V  T  V  W  Q  P  A  F  P  V

        1630                1650                1670
CAGACCACCACTGCCACTACCACCACTGCCCTCCGGGTTAAGAACAAGCCCCTGGGGCCA
Q  T  T  T  A  T  T  T  T  A  L  R  V  K  N  K  P  L  G  P
```

FIG.1J

```
       1690                1710                1730
GCAGGGTCTGAGAATGAAATTCCCACTCATGTTTTGCCACCGTGTGCAAATTTACAGGCA
A  G  S  E  N  E  I  P  T  H  V  L  P  P  C  A  N  L  Q  A

       1750                1770                1790
CAGAAGCTGAAATCCAATGTGTCGGGCAATACACACCTCTGTATTTCCAATGGTAATTAT
Q  K  L  K  S  N  V  S  G  N  T  H  L  C  I  S  N  G  N  Y

       1810                1830                1850
GAAAAAGAAGGTCTCGGTGCTTCCAGCCACATAACCACAAAATCAATGGCTGCTCCTCCA
E  K  E  G  L  G  A  S  S  H  I  T  T  K  S  M  A  A  P  P
```

FIG.1K

```
        1870                1890                1910
AGCTGTGGTCTGAGCCCACTGCTGGTCCTGGTGGTAACCGCTCTGTCCACCCTATTATCT
S  C  G  L  S  P  L  L  V  L  V  V  T  A  L  S  T  L  L  S

        1930                1950                1970
TTAACAGAAACATCATAGCTGCATTAAAAAAATACAATATGGACATGTAAAAAGACAAAA
L  T  E  T  S  *

        1990                2010                2030
ACCAAGTTATCTGTTTCCTGTTCTCTTGTATAGCTGAAATTCCAGTTTAGGAGCTCAGTT

        2050                2070                2090
GAGAAACAGTTCCATTCAACTGGAACATTTTTTTTTT.CCTTTTAAGAAAGCTTCTTGT
```

FIG.1L

```
      2110                2130                2150
GATCCTT.GGGGCTTCTGTGAAAAACCTGATGCAGTGCTCCATCCAAACTCAGAAGGCTT

      2170                2190                2210
TGGGATATGCTGTATTTTAAAGGGACAGTTTGTAACTTGGGCTGTAAAGCAAACTGGGGC

      2230                2250                2270
TGTGTTTTCGATGATGATGAT.ATCATGAT.ATGAT........................

      2290                2310                2330
...............GATTTTAACAGTTTTACTTCTGGCCTTTCCTAGCTAGAGAAGGAG
```

FIG.1M

2350 2370 2390

TTAATATTTCTAAGGTAACTCCCATATCTCCTTTAATGACATTGATTTCTAATGATATAA

2410 2430 2450

ATTTCAGCCTACATTGATGCCAAGCTTTTTTGCCACAAAGAAGATTCTTACCAAGAGTGG

2470 2490 2510

GCTTTGTGGAAACAGCTGGTACTGATGTTCACCTTTATATATGTACTAGCATTTTCCACG

2530 2550

CTGATGTTTATGTACTGTAAACAGTTCTGCACTCTTGTACAAAAGAAAA

FIG.2A

Human Glial Cell Line-Derived
Neurotrophic Factor Receptor Protein

```
M F L A T L Y F A L P L L D L L L S A E  20
V S G G D R L D C V K A S D Q C L K E Q  40
S C S T K Y R T L R Q C V A G K E T N F  60
S L A S G L E A K D E C R S A M E A L K  80
Q K S L Y N C R C K R G M K K E K N C L 100
R I Y W S M Y Q S L Q G N D L L E D S P 120
Y E P V N S R L S D I F R V V P F I S D 140
V F Q Q V E H I P K G N N C L D A A K A 160
C N L D D I C K K Y R S A Y I T P C T T 180
S V S N D V C N R R K C H K A L R Q F F 200
D K V P A K H S Y G M L F C S C R D I A 220
```

FIG.2B

C T E R R R Q T I V P V C S Y E E R E K 240

P N C L N L Q D S C K T N Y I C R S R L 260

A D F F T N C Q P E S R S V S S C L K E 280

N Y A D C L L A Y S G L I G T V M T P N 300

Y I D S S S L S V A P W C D C S N S G N 320

D L E E C L K F L N F F K D N T C L K N 340

A I Q A F G N G S D V T V W Q P A F P V 360

Q T T T A T T T T A L R V K N K P L G P 380

A G S E N E I P T H V L P P C A N L Q A 400

Q K L K S N V S G N T H L C I S N G N Y 420

E K E G L G A S S H I T T K S M A A P P 440

S C G L S P L L V L V V T A L S T L L S 460

L T E T S * 465

FIG.3A

Rat Glial Cell Line-Derived
Neurotrophic Factor Receptor Protein

```
10                             30                             50
AGCTCGCTCTCCCGGGGCAGTGGTGTGGATGCACCGGAGTTCGGGCGCTGGGCAAGTTGG

70                             90                            110
GTCGGAACTGAACCCCTGAAAGCGGGTCCGCCTCCCGCCCTCGCGCCCGCCCGGATCTGA

130                           150                            170
GTCGCTGGCGGCGGTGGGCGGCAGAGCGACGGGGAGTCTGCTCTCACCCTGGATGGAGCT
```

FIG.3B

190 210 230

GAACTTTGAGTGGCCAGAGGAGCGCAGTCGCCCGGGGATCGCTGCACGCTGAGCTCTCTC

250 270 290

CCCGAGACCGGGCGGCGGCTTTGGATTTTGGGGGGGCGGGGACCAGCTGCGCGGCGGCAC

310 330 350

CATGTTCCTAGCCACTCTGTACTTCGCGCTGCCACTCCTGGATTTGCTGATGTCCGCCGA

M F L A T L Y F A L P L L D L L M S A E

370 390 410

GGTGAGTGGTGGAGACCGTCTGGACTGTGTGAAAGCCAGCGATCAGTGCCTGAAGGAACA

V S G G D R L D C V K A S D Q C L K E Q

FIG.3C

```
        430                 450                 470
GAGCTGCAGCACCAAGTACCGCACACTAAGGCAGTGCGTGGCGGGCAAGGAAACCAACTT
 S  C  S  T  K  Y  R  T  L  R  Q  C  V  A  G  K  E  T  N  F

        490                 510                 530
CAGCCTGACATCCGGCCTTGAGGCCAAGGATGAGTGCCGTAGCGCCATGGAGGCCTTGAA
 S  L  T  S  G  L  E  A  K  D  E  C  R  S  A  M  E  A  L  K
```

FIG.3D

```
         550                 570                 590
GCAGAAGTCTCTGTACAACTGCCGCTGCAAGCGGGGCATGAAGAAAGAGAAGAATTGTCT
 Q  K  S  L  Y  N  C  R  C  K  R  G  M  K  K  E  K  N  C  L

         610                 630                 650
GCGTATCTACTGGAGCATGTACCAGAGCCTGCAGGGAAATGACCTCCTGGAAGATTCCCC
 R  I  Y  W  S  M  Y  Q  S  L  Q  G  N  D  L  L  E  D  S  P

         670                 690                 710
GTATGAGCCGGTTAACAGCAGGTTGTCAGATATATTCCGGGCAGTCCCGTTCATATCAGA
 Y  E  P  V  N  S  R  L  S  D  I  F  R  A  V  P  F  I  S  D
```

FIG.3E

```
730                 750                 770
TGTTTTCCAGCAAGTGGAACACATTTCCAAAGGGAACAACTGCCTGGACGCAGCCAAGGC
 V  F  Q  Q  V  E  H  I  S  K  G  N  N  C  L  D  A  A  K  A

790                 810                 830
CTGCAACCTGGACGACACCTGTAAGAAGTACAGGTCGGCCTACATCACCCCCTGCACCAC
 C  N  L  D  D  T  C  K  K  Y  R  S  A  Y  I  T  P  C  T  T

850                 870                 890
CAGCATGTCCAACGAGGTCTGCAACCGCCGTAAGTGCCACAAGGCCCTCAGGCAGTTCTT
 S  M  S  N  E  V  C  N  R  R  K  C  H  K  A  L  R  Q  F  F
```

FIG.3F

```
        910                 930                 950
CGACAAGGTTCCGGCCAAGCACAGCTACGGGATGCTCTTCTGCTCCTGCCGGGACATCGC
 D  K  V  P  A  K  H  S  Y  G  M  L  F  C  S  C  R  D  I  A

        970                 990                1010
CTGCACCGAGCGGCGGCGACAGACTATCGTCCCCGTGTGCTCCTATGAAGAACGAGAGAG
 C  T  E  R  R  R  Q  T  I  V  P  V  C  S  Y  E  E  R  E  R

       1030                1050                1070
GCCCAACTGCCTGAGTCTGCAAGACTCCTGCAAGACCAATTACATCTGCAGATCTCGCCT
 P  N  C  L  S  L  Q  D  S  C  K  T  N  Y  I  C  R  S  R  L
```

FIG.3G

```
       1090                 1110                 1130
TGCAGATTTTTTACCAACTGCCAGCCAGAGTCAAGGTCTGTCAGCAACTGTCTTAAGGA
 A  D  F  F  T  N  C  Q  P  E  S  R  S  V  S  N  C  L  K  E

       1150                 1170                 1190
GAACTACGCAGACTGCCTCCTGGCCTACTCGGGACTGATTGGCACAGTCATGACTCCCAA
 N  Y  A  D  C  L  L  A  Y  S  G  L  I  G  T  V  M  T  P  N

       1210                 1230                 1250
CTACGTAGACTCCAGCAGCCTCAGCGTGGCACCATGGTGTGACTGCAGCAACAGCGGCAA
 Y  V  D  S  S  S  L  S  V  A  P  W  C  D  C  S  N  S  G  N
```

FIG.3H

```
     1270                1290                1310
TGACCTGGAAGACTGCTTGAAATTTCTGAATTTTTTTAAGGACAATACTTGTCTCAAAAA
 D  L  E  D  C  L  K  F  L  N  F  F  K  D  N  T  C  L  K  N

     1330                1350                1370
TGCAATTCAAGCCTTTGGCAATGGCTCAGATGTGACCATGTGGCAGCCAGCCCCTCCAGT
 A  I  Q  A  F  G  N  G  S  D  V  T  M  W  Q  P  A  P  P  V

     1390                1410                1430
CCAGACCACCACTGCCACCACTACCACTGCCTTCCGGGTCAAGAACAAGCCTCTGGGGCC
 Q  T  T  T  A  T  T  T  T  A  F  R  V  K  N  K  P  L  G  P
```

FIG.3I

```
      1450                1470                1490
AGCAGGGTCTGAGAATGAGATCCCCACACACGTTTTACCACCCTGTGCGAATTTGCAGGC
 A  G  S  E  N  E  I  P  T  H  V  L  P  P  C  A  N  L  Q  A

      1510                1530                1550
TCAGAAGCTGAAATCCAATGTGTCGGGTAGCACACACCTCTGTCTTTCTGATAGTGATTT
 Q  K  L  K  S  N  V  S  G  S  T  H  L  C  L  S  D  S  D  F

      1570                1590                1610
CGGAAAGGATGGTCTCGCTGGTGCCTCCAGCCACATAACCACAAAATCAATGGCTGCTCC
 G  K  D  G  L  A  G  A  S  S  H  I  T  T  K  S  M  A  A  P
```

FIG.3J

```
        1630                1650                1670
TCCCAGCTGCAGTCTGAGCTCACTGCCGGTGCTGATGCTCACCGCCCTTGCTGCCCTGTT
 P  S  C  S  L  S  S  L  P  V  L  M  L  T  A  L  A  A  L  L

        1690                1710                1730
ATCTGTATCGTTGGCAGAAACGTCGTAGCTGCATCCGGGAAAACAGTATGAAAAGACAAA
 S  V  S  L  A  E  T  S  *

        1750                1770                1790
AGAGAACCAAGTATTCTGTCCCTGTCCTCTTGTATATCTGAAAATCCAGTTTTAAAAGCT

        1810                1830                1850
CCGTTGAGAAGCAGTTTCACCCAACTGGAACTCTTTCCTTGTTTTTAAGAAAGCTTGTGG
```

FIG.3K

1870 1890 1910

CCCTCAGGGGCTTCTGTTGAAGAACTGCTACAGGGCTAATTCCAAACCCATAAGGCTCTG

1930 1950 1970

GGGCGTGGTGCGGCTTAAGGGGACCATTTGCACCATGTAAAGCAAGCTGGGCTTATCATG

1990 2010 2030

TGTTTGATGGTGAGGATGGTAGTGGTGATGATGATGGTAATTTTAACAGCTTGAACCCTG

2050 2070 2090

TTCTCTCTACTGGTTAGGAACAGGAGATACTATTGATAAAGATTCTTCCATGTCTTACTC

2110 2130

AGCAGCATTGCCTTCTGAAGACAGGCCCGCAGCCGTCG

FIG.4A

Rat Glial Cell Line-Derived
Neurotrophic Factor Receptor Protein

M F L A T L Y F A L P L L D L L M S A E 20

V S G G D R L D C V K A S D Q C L K E Q 40

S C S T K Y R T L R Q C V A G K E T N F 60

S L T S G L E A K D E C R S A M E A L K 80

Q K S L Y N C R C K R G M K K E K N C L 100

R I Y W S M Y Q S L Q G N D L L E D S P 120

Y E P V N S R L S D I F R A V P F I S D 140

V F Q Q V E H I S K G N N C L D A A K A 160

C N L D D T C K K Y R S A Y I T P C T T 180

S M S N E V C N R R K C H K A L R Q F F 200

D K V P A K H S Y G M L F C S C R D I A 220

C T E R R R Q T I V P V C S Y E E R E R 240

FIG.4B

P N C L S L Q D S C K T N Y I C R S R L 260

A D F F T N C Q P E S R S V S N C L K E 280

N Y A D C L L A Y S G L I G T V M T P N 300

Y V D S S S L S V A P W C D C S N S G N 320

D L E D C L K F L N F F K D N T C L K N 340

A I Q A F G N G S D V T M W Q P A P P V 360

Q T T T A T T T T A F R V K N K P L G P 380

A G S E N E I P T H V L P P C A N L Q A 400

Q K L K S N V S G S T H L C L S D S D F 420

G K D G L A G A S S H I T T K S M A A P 440

P S C S L S S L P V L M L T A L A A L L 460

S V S L A E T S * 468

FIG. 5A

Human GDNF receptor Clones -- Alignment to generate consensus sequence

```
                              -237                                                -188
(SEQ ID NO:45)      Gdnfr   AATCTGGCCT CGGAACACGC CATTCTCCGC GCCGCTTCCA ATAACCACTA
(SEQ ID NO:46)  Hsgr-21af     TCTGGCCT CGGAACACGC CATTCTCCGC GCCGCTTCCA ATAACCACTA
(SEQ ID NO:47)  Hsgr-21bf   AATCTGGCCT CGGAACACGC CATTCTCCGC GCCGCTTCCA ATAACCACTA
(SEQ ID NO:48)     21acon     TCTGGCCT CGGAACACGC CATTCTCCGC GCCGCTTCCA ATAACCACTA
(SEQ ID NO:49)     21bcon   AATCTGGCCT CGGAACACGC CATTCTCCGC GCCGCTTCCA ATAACCACTA

                              -187                                                -138
(SEQ ID NO:45)      Gdnfr   ACATCCCTAA CGAGCATCCG AGCCGAGGGC TCTGCTCGGA AATCGTCCTG
(SEQ ID NO:46)  Hsgr-21af   ACATCCCTAA CGAGCATCCG AGCCGAGGGC TCTGCTCGGA AATCGTCCTG
(SEQ ID NO:47)  Hsgr-21bf   ACATCCCTAA CGAGCATCCG AGCCGAGGGC TCTGCTCGGA AATCGTCCTG
(SEQ ID NO:48)     21acon   ACATCCCTAA CGAGCATCCG AGCCGAGGGC TCTGCTCGGA AATCGTCCTG
(SEQ ID NO:49)     21bcon   ACATCCCTAA CGAGCATCCG AGCCGAGGGC TCTGCTCGGA AATCGTCCTG

                              -137                                                 -88
(SEQ ID NO:45)      Gdnfr   GCCCAACTCG GCCCTTCGAG CTCTCGAAGA TTACCGCATC TATTTTTTTT
(SEQ ID NO:46)  Hsgr-21af   GCCCAACTCG GCCCTTCGAG CTCTCGAAGA TTACCGCATC TATTTTTTTT
(SEQ ID NO:47)  Hsgr-21bf   GCCCAACTCG GCCCTTCGAG CTCTCGAAGA TTACCGCATC TATTTTTTTT
(SEQ ID NO:48)     21acon   GCCCAACTCG GCCCTTCGAG CTCTCGAAGA TTACCGCATC TATTTTTTTT
(SEQ ID NO:49)     21bcon   GCCCAACTCG GCCCTTCGAG CTCTCGAAGA TTACCGCATC TATTTTTTTT
```

FIG. 5B

```
                                  -87                                                 -38
(SEQ ID NO:45)        Gdnfr   TTCTTTTTTT TCTTTTCCTA GCGCAGATAA AGTGAGCCCG GAAAGGGAAG
(SEQ ID NO:46)   Hsgr-21af   TTCTTTTTTT TCTTTTCCTA GCGCAGATAA AGTGAGCCCG GAAAGGGAAG
(SEQ ID NO:47)   Hsgr-21bf   TTCTTTTTTT TCTTTTCCTA GCGCAGATAA AGTGAGCCCG GAAAGGGAAG
(SEQ ID NO:48)      21acon   TTCTTTTTTT TCTTTTCCTA GCGCAGATAA AGTGAGCCCG GAAAGGGAAG
(SEQ ID NO:49)      21bcon   TTCTTTTTTT TCTTTTCCTA GCGCAGATAA AGTGAGCCCG GAAAGGGAAG

                                  -37                                                  12
(SEQ ID NO:45)        Gdnfr   GAGGGGGCGG GGACACCATT GCCCTGAAAG AATAAATAAG TAAATAAACA
(SEQ ID NO:46)   Hsgr-21af   GAGGGGGCGG GGACACCATT GCCCTGAAAG AATAAATAAG TAAATAAACA
(SEQ ID NO:47)   Hsgr-21bf   GAGGGGGCGG GGACACCATT GCCCTGAAAG AATAAATAAG TAAATAAACA
(SEQ ID NO:48)      21acon   GAGGGGGCGG GGACACCATT GCCCTGAAAG AATAAATAAG TAAATAAACA
(SEQ ID NO:49)      21bcon   GAGGGGGCGG GGACACCATT GCCCTGAAAG AATAAATAAG TAAATAAACA

                                  13                                                   62
(SEQ ID NO:45)        Gdnfr   AACTGGCTCC TCGCCGCAGC TGGACGCGGT CGGTTGAGTC CAGGTTGGGT
(SEQ ID NO:46)   Hsgr-21af   AACTGGCTCC TCGCCGCAGC TGGACGCGGT CGGTTGAGTC CAGGTTGGGT
(SEQ ID NO:47)   Hsgr-21bf   AACTGGCTCC TCGCCGCAGC TGGACGCGGT CGGTTGAGTC CAGGTTGGGT
(SEQ ID NO:48)      21acon   AACTGGCTCC TCGCCGCAGC TGGACGCGGT CGGTTGAGTC CAGGTTGGGT
(SEQ ID NO:49)      21bcon   AACTGGCTCC TCGCCGCAGC TGGACGCGGT CGGTTGAGTC CAGGTTGGGT

                                  63                                                  112
(SEQ ID NO:45)        Gdnfr   CGGACCTGAA CCCCTAAAAG CGGAACCGCC TCCCGCCCTC GCCATCCCGG
(SEQ ID NO:46)   Hsgr-21af   CGGACCTGAA CCCCTAAAAG CGGAACCGCC TCCCGCCCTC GCCATCCCGG
(SEQ ID NO:47)   Hsgr-21bf   CGGACCTGAA CCCCTAAAAG CGGAACCGCC TCCCGCCCTC GCCATCCCGG
(SEQ ID NO:48)      21acon   CGGACCTGAA CCCCTAAAAG CGGAACCGCC TCCCGCCCTC GCCATCCCGG
(SEQ ID NO:49)      21bcon   CGGACCTGAA CCCCTAAAAG CGGAACCGCC TCCCGCCCTC GCCATCCCGG
```

FIG. 5C

```
                             113                                                162
(SEQ ID NO:45)      Gdnfr   AGCTGAGTCG CCGGCGGCGG TGGCTGCTGC CAGACCCGGA GTTTCCTCTT
(SEQ ID NO:46)  Hsgr-21af   AGCTGAGTCG CCGGCGGCGG TGGCTGCTGC CAGACCCGGA GTTTCCTCTT
(SEQ ID NO:47)  Hsgr-21bf   AGCTGAGTCG CCGGCGGCGG TGGCTGCTGC CAGACCCGGA GTTTCCTCTT
(SEQ ID NO:48)     21acon   AGCTGAGTCG CCGGCGGCGG TGGCTGCTGC CAGACCCGGA GTTTCCTCTT
(SEQ ID NO:49)     21bcon   AGCTGAGTCG CCGGCGGCGG TGGCTGCTGC CAGACCCGGA GTTTCCTCTT

                             163                                                212
(SEQ ID NO:45)      Gdnfr   TCACTGGATG GAGCTGAACT TTGGGCGGCC AGAGCAGCAC AGCTGTCCGG
(SEQ ID NO:46)  Hsgr-21af   TCACTGGATG GAGCTGAACT TTGGGCGGCC AGAGCAGCAC AGCTGTCCGG
(SEQ ID NO:47)  Hsgr-21bf   TCACTGGATG GAGCTGAACT TTGGGCGGCC AGAGCAGCAC AGCTGTCCGG
(SEQ ID NO:48)     21acon   TCACTGGATG GAGCTGAACT TTGGGCGGCC AGAGCAGCAC AGCTGTCCGG
(SEQ ID NO:49)     21bcon   TCACTGGATG GAGCTGAACT TTGGGCGGCC AGAGCAGCAC AGCTGTCCGG

                             213                                                262
(SEQ ID NO:45)      Gdnfr   GGATCGCTGC ACGCTGAGCT CCCTCGGCAA GACCCAGCGG CGGCTCGGGA
(SEQ ID NO:46)  Hsgr-21af   GGATCGCTGC ACGCTGAGCT CCCTCGGCAA GACCCAGCGG CGGCTCGGGA
(SEQ ID NO:47)  Hsgr-21bf   GGATCGCTGC ACGCTGAGCT CCCTCGGCAA GACCCAGCGG CGGCTCGGGA
(SEQ ID NO:48)     21acon   GGATCGCTGC ACGCTGAGCT CCCTCGGCAA GACCCAGCGG CGGCTCGGGA
(SEQ ID NO:49)     21bcon   GGATCGCTGC ACGCTGAGCT CCCTCGGCAA GACCCAGCGG CGGCTCGGGA

                             263                                                312
(SEQ ID NO:45)      Gdnfr   TTTTTTTGGG GGGGCGGGGA CCAGCCCCGC GCCGGCACCA TGTTCCTGGC
(SEQ ID NO:46)  Hsgr-21af   TTTTTTTGGG
(SEQ ID NO:47)  Hsgr-21bf   TTTTTTTGGG
(SEQ ID NO:48)     21acon   TTTTTTTGGG GGGGCGGGGA CCAGCCCCGC GCCGGCACCA TGTTCCTGGC
(SEQ ID NO:49)     21bcon   TTTTTTTGGG GGGGCGGGGA CCAGCCCCGC GCCGGCACCA TGTTCCTGGC
```

FIG. 5D

```
                                313                                                  362
(SEQ ID NO:45)        Gdnfr   GACCCTGTAC TTCGCGCTGC CGCTCTTGGA CTTGCTCCTG TCGGCCGAAG
(SEQ ID NO:48)       21acon   GNCCCTGTAC TTCGCGCTGC CGCTCTTGGA CTTGCTCCTG TCGGCCGAAG
(SEQ ID NO:49)       21bcon   GACCCTGTAC TTCGCGCTGC CGCTCTTGGA CTTGCTCCTG TCGGCCGAAG

                                363                                                  412
(SEQ ID NO:45)        Gdnfr   TGAGCGGCGG AGACCGCCTG GATTGCGTGA AAGCCAGTGA TCAGTGCCTG
(SEQ ID NO:48)       21acon   TGAGCGGCGG AGACCGCCTG GATTGCGTGA AAGCCAGTGA TCAGTGCCTG
(SEQ ID NO:49)       21bcon   TGAGCGGCGG AGACCGCCTG GATTGCGTGA AAGCCAGTGA TCAGTGCCTG

                                413                                                  462
(SEQ ID NO:45)        Gdnfr   AAGGAGCAGA GCTGCAGCAC CAAGTACCGC ACGCTAAGGC AGTGCGTGGC
(SEQ ID NO:48)       21acon   AAGGAGCAGA GCTGCAGCAC CAAGTACCGC ACGCTAAGGC AGTGCGTGGC
(SEQ ID NO:49)       21bcon   AAGGAGCAGA GCTGCAGCAC CAAGTACCGC ACGCTAAGGC AGTGCGTGGC

                                463                                                  512
(SEQ ID NO:45)        Gdnfr   GGGCAAGGAG ACCAACTTCA GCCTGGCATC CGGCCTGGAG GCCAAGGATG
(SEQ ID NO:48)       21acon   GGGCAAGGAG ACCAACTTCA GCCTGGCATC CGGCCTGGAG GCCAAGGATG
(SEQ ID NO:49)       21bcon   GGGCAAGGAG ACCAACTTCA GCCTGGCATC CGGCCTGGAG GCCAAGGATG

                                513                                                  562
(SEQ ID NO:45)        Gdnfr   AGTGCCGCAG CGCCATGGAG GCCCTGAAGC AGAAGTCGCT CTACAACTGC
(SEQ ID NO:48)       21acon   AGTGCCGCAG CGCCATGGAG GCCCTGAAGC AGAAGTCGCT CTACAACTGC
(SEQ ID NO:49)       21bcon   AGTGCCGCAG CGCCATGGAG GCCCTGAAGC AGAAGTCGCT CTACAACTGC
```

FIG. 5E

```
                          563                                          612
(SEQ ID NO:45)    Gdnfr   CGCTGCAAGC GGGGTATGAA GAAGGAGAAG AACTGCCTGC GCATTTACTG
(SEQ ID NO:48)   21acon   CGCTGCAAGC GGGGTATGAA GAAGGAGAAG AACTGCCTGC GCATTTACTG
(SEQ ID NO:49)   21bcon   CGCTGCAAGC GGGGTATGAA GAAGGAGAAG AACTGCCTGC GCATTTACTG

                          613                                          662
(SEQ ID NO:45)    Gdnfr   GAGCATGTAC CAGAGCCTGC AGGGAAATGA TCTGCTGGAG GATTCCCCAT
(SEQ ID NO:48)   21acon   GAGCATGTAC CAGAGCCTGC AGGGAAATGA TCTGCTGGAG GATTCCCCAT
(SEQ ID NO:49)   21bcon   GAGCATGTAC CAGAGCCTGC AGGGAAATGA TCTGCTGGAG GATTCCCCAT

                          663                                          712
(SEQ ID NO:45)    Gdnfr   ATGAACCAGT TAACAGCAGA TTGTCAGATA TATTCCGGGT GGTCCCATTC
(SEQ ID NO:48)   21acon   ATGAACCAGT TAACAGCAGA TTGTCAGATA TATTCCGGGT GGTCCCATTC
(SEQ ID NO:49)   21bcon   ATGAACCAGT TAACAGCAGA TTGTCAGATA TATTCCGGGT GGTCCCATTC

                          713                                          762
(SEQ ID NO:45)    Gdnfr   ATATCAGATG TTTTTCAGCA AGTGGAGCAC ATTCCCAAAG GGAACAACTG
(SEQ ID NO:48)   21acon   ATATCAGATG TTTTTCAGCA AGTGGAGCAC ATTCCCAAAG GGAACAACTG
(SEQ ID NO:49)   21bcon   ATATCAGATG TTTTTCAGCA AGTGGAGCAC ATTCCCAAAG GGAACAACTG

                          763                                          812
(SEQ ID NO:45)    Gdnfr   CCTGGATGCA GCGAAGGCCT GCAACCTCGA CGACATTTGC AAGAAGTACA
(SEQ ID NO:48)   21acon   CCTGGATGCA GCGAAGGCCT GCAACCTCGA CGACATTTGC AAGAAGTACA
(SEQ ID NO:49)   21bcon   CCTGGATGCA GCGAAGGCCT GCAACCTCGA CGACATTTGC AAGAAGTACA
```

FIG. 5F

```
                                 813                                              862
(SEQ ID NO:45)       Gdnfr   GGTCGGCGTA CATCACCCCG TGCACCACCA GCGTGTCCAA .GATGTCTGC
(SEQ ID NO:50)    Hsgr-29a    GTCGGCGTA CATCACCCCG TGCACCACCA GCGTGTCCAA TGATGTCTGC
(SEQ ID NO:48)      21acon   GGTCGGCGTA CATCACCCCG TGCACCACCA GCGTGTCCAA CGATGTCTGC
(SEQ ID NO:49)      21bcon   GGTCGGCGTA CATCACCCCG TGCACCACCA GCGTGTCCAA CGATGTCTGC
(SEQ ID NO:51)       29brc    GTCGGCGTA CATCACCCCG TGCACCACCA GCGTGTCCAA TGATGTCTGC

                                 863                                              912
(SEQ ID NO:45)       Gdnfr   AACCGCCGCA AGTGCCACAA GGCCCTCCGG CAGTTCTTTG ACAAGGTCCC
(SEQ ID NO:50)    Hsgr-29a   AACCGCCGCA AGTGCCACAA GGCCCTCCGG CAGTTCTTTG ACAAGGTCCC
(SEQ ID NO:48)      21acon   AACCGCCGCA AGTGCCACAA GGCCCTCCGG CAGTTCTTTG ACAAGGTCCC
(SEQ ID NO:49)      21bcon   AACCGCCGCA AGTGCCACAA GGCCCTCCGG CAGTTCTTTG ACAAGGTCCC
(SEQ ID NO:51)       29brc   AACCGCCGCA AGTGCCACAA GGCCCTCCGG CAGTTCTTTG ACAAGGTCCC

                                 913                                              962
(SEQ ID NO:45)       Gdnfr   GGCCAAGCAC AGCTACGGAA TGCTCTTCTG CTCCTGCCGG GACATCGCCT
(SEQ ID NO:50)    Hsgr-29a   GGCCAAGCAC AGCTACGGAA TGCTCTTCTG CTCCTGCCGG GACATCGCCT
(SEQ ID NO:48)      21acon   GGCCAAGCAC AGCTACGGAA TGCTCTTCTG CTCCTGCCGG GACATCGCCT
(SEQ ID NO:49)      21bcon   GGCCAAGCAC AGCTACGGAA TGCTCTTCTG CTCCTGCCGG GACATCGCCT
(SEQ ID NO:51)       29brc   GGCCAAGCAC AGCTACGGAA TGCTCTTCTG CTCCTGCCGG GACATCGCCT

                                 963                                             1012
(SEQ ID NO:45)       Gdnfr   GCACAGAGCG GAGGCGACAG ACCATCGTGC CTGTGTGCTC CTATGAAGAG
(SEQ ID NO:50)    Hsgr-29a   GCACAGAGCG GAGGCGACAG ACCATCGTGC CTGTGTGCTC CTATGAAGAG
(SEQ ID NO:48)      21acon   GCACAGAGCG GAGGCGACAG ACCATCGTGC CTGTGTGCTC CTATGAAGAG
(SEQ ID NO:49)      21bcon   GCACAGAGCG GAGGCGACAG ACCATCGTGC CTGTGTGCTC CTATGAAGAG
(SEQ ID NO:51)       29brc   GCACAGAGCG GAGGCGACAG ACCATCGTGC CTGTGTGCTC CTATGAAGAG
```

FIG. 5G

```
                             1013                                                1062
(SEQ ID NO:45)      Gdnfr   AGGGAGAAGC CCAACTGTTT GAATTTGCAG GACTCCTGCA AGACGAATTA
(SEQ ID NO:52)  Hsgr-21ar                         GAATTTGCAG GACTCCTGCA AGACGAATTA
(SEQ ID NO:53)  Hsgr-21br                                                        A
(SEQ ID NO:50)   Hsgr-29a   AGGGAGAAGC CCAACTGTTT GAATTTGCAG GACTCCTGCA AGACGAATTA
(SEQ ID NO:48)     21acon   AGGGAGAAGC CCAACTGTTT GAATTTGCAG GACTCCTGCA AGACGAATTA
(SEQ ID NO:49)     21bcon   AGGGAGAAGC CCAACTGTTT GAATTTGCAG GACTCCTGCA AGACGAATTA
(SEQ ID NO:51)      29brc   AGGGAGAAGC CCAACTGTTT GAATTTGCAG GACTCCTGCA AGACGAATTA

                             1063                                                1112
(SEQ ID NO:45)      Gdnfr   CATCTGCAGA TCTCGCCTTG CGGATTTTTT TACCAACTGC CAGCCAGAGT
(SEQ ID NO:52)  Hsgr-21ar   CATCTGCAGA TCTCGCCTTG CGGATTTTTT TACCAACTGC CAGCCAGAGT
(SEQ ID NO:53)  Hsgr-21br   CATCTGCAGA TCTCGCCTTG CGGATTTTTT TACCAACTGC CAGCCAGAGT
(SEQ ID NO:50)   Hsgr-29a   CATCTGCAGA TCTCGCCTTG CGGATTTTTT TACCAACTGC CAGCCAGAGT
(SEQ ID NO:48)     21acon   CATCTGCAGA TCTCGCCTTG CGGATTTTTT TACCAACTGC CAGCCAGAGT
(SEQ ID NO:49)     21bcon   CATCTGCAGA TCTCGCCTTG CGGATTTTTT TACCAACTGC CAGCCAGAGT
(SEQ ID NO:51)      29brc   CATCTGCAGA TCTCGCCTTG CGGATTTTTT TACCAACTGC CAGCCAGAGT

                             1113                                                1162
(SEQ ID NO:45)      Gdnfr   CAAGGTCTGT CAGCAGCTGT CTAAAGGAAA ACTACGCTGA CTGCCTCCTC
(SEQ ID NO:52)  Hsgr-21ar   CAAGGTCTGT CAGCAGCTGT CTAAAGGAAA ACTACGCTGA CTGCCTCCTC
(SEQ ID NO:53)  Hsgr-21br   CAAGGTCTGT CAGCAGCTGT CTAAAGGAAA ACTACGCTGA CTGCCTCCTC
(SEQ ID NO:50)   Hsgr-29a   CAAGGTCTGT CAGCAGCTGT CTAAAGGAAA ACTACGCTGA CTGCCTCCTC
(SEQ ID NO:48)     21acon   CAAGGTCTGT CAGCAGCTGT CTAAAGGAAA ACTACGCTGA CTGCCTCCTC
(SEQ ID NO:49)     21bcon   CAAGGTCTGT CAGCAGCTGT CTAAAGGAAA ACTACGCTGA CTGCCTCCTC
(SEQ ID NO:51)      29brc   CAAGGTCTGT CAGCAGCTGT CTAAAGGAAA ACTACGCTGA CTGCCTCCTC
```

FIG. 5H

```
                             1163                                             1212
(SEQ ID NO:45)      Gdnfr  GCCTACTCGG GGCTTATTGG CACAGTCATG ACCCCCAACT ACATAGACTC
(SEQ ID NO:52)  Hsgr-21ar  GCCTACTCGG GGCTTATTGG CACAGTCATG ACCCCCAACT ACATAGACTC
(SEQ ID NO:53)  Hsgr-21br  GCCTACTCGG GGCTTATTGG CACAGTCATG ACCCCCAACT ACATAGACTC
(SEQ ID NO:50)   Hsgr-29a  GCCTACTCGG GGCTTATTGG CACAGTCATG ACCCCCAACT ACATAGACTC
(SEQ ID NO:48)     21acon  GCCTACTCGG GGCTTATTGG CACAGTCATG ACCCCCAACT ACATAGACTC
(SEQ ID NO:49)     21bcon  GCCTACTCGG GGCTTATTGG CACAGTCATG ACCCCCAACT ACATAGACTC
(SEQ ID NO:51)      29brc  GCCTACTCGG GGCTTATTGG CACAGTCATG ACCCCCAACT ACATAGACTC
                             1213                                             1262
(SEQ ID NO:45)      Gdnfr  CAGTAGCCTC AGTGTGGCCC CATGGTGTGA CTGCAGCAAC AGTGGGAACG
(SEQ ID NO:54)     Hsgr-2                                                TGGGAACG
(SEQ ID NO:52)  Hsgr-21ar  CAGTAGCCTC AGTGTGGCCC CATGGTGTGA CTGCAGCAAC AGTGGGAACG
(SEQ ID NO:53)  Hsgr-21br  CAGTAGCCTC AGTGTGGCCC CATGGTGTGA CTGCAGCAAC AGTGGGAACG
(SEQ ID NO:50)   Hsgr-29a  CAGTAGCCTC AGTGTGGCCC CATGGTGTGA CTGCAGCAAC AGTGGGAACG
(SEQ ID NO:48)     21acon  CAGTAGCCTC AGTGTGGCCC CATGGTGTGA CTGCAGCAAC AGTGGGAACG
(SEQ ID NO:49)     21bcon  CAGTAGCCTC AGTGTGGCCC CATGGTGTGA CTGCAGCAAC AGTGGGAACG
(SEQ ID NO:51)      29brc  CAGTAGCCTC AGTGTGGCCC CATGGTGTGA CTGCAGCAAC AGTGGGAACG
```

FIG. 5I

```
                               1263                                               1312
(SEQ ID NO:45)       Gdnfr   ACCTAGAAGA GTGCTTGAAA TTTTTGAATT TCTTCAAGGA CAATACATGT
(SEQ ID NO:54)      Hsgr-2   ACCTAGAAGA GTGCTTGAAA TTTTTGAATT TCTTCAAGGA CAATACATGT
(SEQ ID NO:55)      Hsgr-9            A GTGCTTGAAA TTTTTGAATT TCTTCAAGGA CAATACATGT
(SEQ ID NO:52)  Hsgr-21ar   ACCTAGAAGA GTGCTTGAAA TTTTTGAATT TCTTCAAGGA CAATACATGT
(SEQ ID NO:53)  Hsgr-21br   ACCTAGAAGA GTGCTTGAAA TTTTTGAATT TCTTCAAGGA CAATACATGT
(SEQ ID NO:50)   Hsgr-29a   ACCTAGAAGA GTGCTTGAAA TTTTTGAATT TCTTCAAGGA CAATACATGT
(SEQ ID NO:48)     21acon   ACCTAGAAGA GTGCTTGAAA TTTTTGAATT TCTTCAAGGA CAATACATGT
(SEQ ID NO:49)     21bcon   ACCTAGAAGA GTGCTTGAAA TTTTTGAATT TCTTCAAGGA CAATACATGT
(SEQ ID NO:51)      29brc   ACCTAGAAGA GTGCTTGAAA TTTTTGAATT TCTTCAAGGA CAATACATGT

                               1313                                               1362
(SEQ ID NO:45)       Gdnfr   CTTAAAAATG CAATTCAAGC CTTTGGCAAT GGCTCCGATG TGACCGTGTG
(SEQ ID NO:54)      Hsgr-2   CTTAAAAATG CAATTCAAGC CTTTGGCAAT GGCTCCGATG TGACCGTGTG
(SEQ ID NO:55)      Hsgr-9   CTTAAAAATG CAATTCAAGC CTTTGGCAAT GGCTCCGATG TGACCGTGTG
(SEQ ID NO:52)  Hsgr-21ar   CTTAAAAATG CAATTCAAGC CTTTGGCAAT GGCTCCGATG TGACCGTGTG
(SEQ ID NO:53)  Hsgr-21br   CTTAAAAATG CAATTCAAGC CTTTGGCAAT GGCTCCGATG TGACCGTGTG
(SEQ ID NO:50)   Hsgr-29a   CTTAAAAATG CAATTCAAGC CTTTGGCAAT GGCTCCGATG TGACCGTGTG
(SEQ ID NO:48)     21acon   CTTAAAAATG CAATTCAAGC CTTTGGCAAT GGCTCCGATG TGACCGTGTG
(SEQ ID NO:49)     21bcon   CTTAAAAATG CAATTCAAGC CTTTGGCAAT GGCTCCGATG TGACCGTGTG
(SEQ ID NO:51)      29brc   CTTAAAAATG CAATTCAAGC CTTTGGCAAT GGCTCCGATG TGACCGTGTG
```

FIG. 5J

```
                                1363                                              1412
(SEQ ID NO:45)       Gdnfr  GCAGCCAGCC TTCCCAGTAC AGACCACCAC TGCCaCTACC ACCACTGCCC
(SEQ ID NO:54)      Hsgr-2  GCAGCCAGCC TTCCCAGTAC AGACCACCAC TGCCACTACC ACCACTGCCC
(SEQ ID NO:55)      Hsgr-9  GCAGCCAGCC TTCCCAGTAC AGACCACCAC TGCCACTACC ACCACTGCCC
(SEQ ID NO:52)  Hsgr-21ar   GCAGCCAGCC TTCCCAGTAC AGACCACCAC TGCCACTACC ACCACTGCCC
(SEQ ID NO:53)  Hsgr-21br   GCAGCCAGCC TTCCCAGTAC AGACCACCAC TGCCACTACC ACCACTGCCC
(SEQ ID NO:50)   Hsgr-29a   GCAGCCAGCC TTCCCAGTAC AGACCACCAC TGCCGCTACC ACCACTGCCC
(SEQ ID NO:48)      21acon  GCAGCCAGCC TTCCCAGTAC AGACCACCAC TGCCACTACC ACCACTGCCC
(SEQ ID NO:49)      21bcon  GCAGCCAGCC TTCCCAGTAC AGACCACCAC TGCCACTACC ACCACTGCCC
(SEQ ID NO:51)       29brc  GCAGCCAGCC TTCCCAGTAC AGACCACCAC TGCCGCTACC ACCACTGCCC

                                1413                                              1462
(SEQ ID NO:45)       Gdnfr  TCCGGGTTAA GAACAAGCCC CTGGGGCCAG CAGGGTCTGA GAATGAAATT
(SEQ ID NO:54)      Hsgr-2  TCCGGGTTAA GAACAAGCCC CTGGGGCCAG CAGGGTCTGA GAATGAAATT
(SEQ ID NO:55)      Hsgr-9  TCCGGGTTAA GAACAAGCCC CTGGGGCCAG CAGGGTCTGA GAATGAAATT
(SEQ ID NO:52)  Hsgr-21ar   TCCGGGTTAA GAACAAGCCC CTGGGGCCAG CAGGGTCTGA GAATGAAATT
(SEQ ID NO:53)  Hsgr-21br   TCCGGGTTAA GAACAAGCCC CTGGGGCCAG CAGGGTCTGA GAATGAAATT
(SEQ ID NO:50)   Hsgr-29a   TCCGGGTTAA GAACAAGCCC CTGGGGCCAG CAGGGTCTGA GAATGAAATT
(SEQ ID NO:48)      21acon  TCCGGGTTAA GAACAAGCCC CTGGGGCCAG CAGGGTCTGA GAATGAAATT
(SEQ ID NO:49)      21bcon  TCCGGGTTAA GAACAAGCCC CTGGGGCCAG CAGGGTCTGA GAATGAAATT
(SEQ ID NO:51)       29brc  TCCGGGTTAA GAACAAGCCC CTGGGGCCAG CAGGGTCTGA GAATGAAATT
```

FIG. 5K

```
                                1463                                                1512
(SEQ ID NO:45)      Gdnfr  CCCACTCATG TTTTGCCACC GTGTGCAAAT TTACAGGCAC AGAAGCTGAA
(SEQ ID NO:54)     Hsgr-2  CCCACTCATG TTTTGCCACC GTGTGCAAAT TTACAGGCAC AGAAGCTGAA
(SEQ ID NO:55)     Hsgr-9  CCCACTCATG TTTTGCCACC GTGTGCAAAT TTACAGGCAC AGAAGCTGAA
(SEQ ID NO:52) Hsgr-21ar  CCCACTCATG TTTTGCCACC GTGTGCAAAT TTACAGGCAC AGAAGCTGAA
(SEQ ID NO:53) Hsgr-21br  CCCACTCATG TTTTGCCACC GTGTGCAAAT TTACAGGCAC AGAAGCTGAA
(SEQ ID NO:50)  Hsgr-29a  CCCACTCATG TTTTGCCACC GTGTGCAAAT TTACAGGCAC AGAAGCTGAA
(SEQ ID NO:48)    21acon  CCCACTCATG TTTTGCCACC GTGTGCAAAT TTACAGGCAC AGAAGCTGAA
(SEQ ID NO:49)    21bcon  CCCACTCATG TTTTGCCACC GTGTGCAAAT TTACAGGCAC AGAAGCTGAA
(SEQ ID NO:51)     29brc  CCCACTCATG TTTTGCCACC GTGTGCAAAT TTACAGGCAC AGAAGCTGAA

                                1513                                                1562
(SEQ ID NO:45)      Gdnfr  ATCCAATGTG TCGGGCAATA CACACCTCTG TATTTCCAAT GGTAATTATG
(SEQ ID NO:54)     Hsgr-2  ATCCAATGTG TCGGGCAATA CACACCTCTG TATTTCCAAT GGTAATTATG
(SEQ ID NO:55)     Hsgr-9  ATCCAATGTG TCGGGCAATA CACACCTCTG TATTTCCAAT GGTAATTATG
(SEQ ID NO:52) Hsgr-21ar  ATCCAATGTG TCGGGCAATA CACACCTCTG TATTTCCAAT GGTAATTATG
(SEQ ID NO:53) Hsgr-21br  ATCCAATGTG TCGGGCAATA CACACCTCTG TATTTCCAAT GGTAATTATG
(SEQ ID NO:48)    21acon  ATCCAATGTG TCGGGCAATA CACACCTCTG TATTTCCAAT GGTAATTATG
(SEQ ID NO:49)    21bcon  ATCCAATGTG TCGGGCAATA CACACCTCTG TATTTCCAAT GGTAATTATG
(SEQ ID NO:51)     29brc  ATCCAATGTG TCGGGCAATA CACACCTCTG TATTTCCAAT GGTAATTATG
```

FIG. 5L

```
                              1563                                               1612
(SEQ ID NO:45)      Gdnfr   AAAAAGAAGG TCTCGGTGCT TCCAGCCACA TAACCACAAA ATCAATGGCT
(SEQ ID NO:54)     Hsgr-2   AAAAAGAAGG TCTCGGTGCT TCCAGCCACA TAACCACAAA ATCAATGGCT
(SEQ ID NO:55)     Hsgr-9   AAAAAGAAGG TCTCGGTGCT TCCAGCCACA TAACCACAAA ATCAATGGCT
(SEQ ID NO:52)  Hsgr-21ar   AAAAAGAAGG TCTCGGTGCT TCCAGCCACA TAACCACAAA ATCAATGGCT
(SEQ ID NO:53)  Hsgr-21br   AAAAAGAAGG TCTCGGTGCT TCCAGCCACA TAACCACAAA ATCAATGGCT
(SEQ ID NO:48)     21acon   AAAAAGAAGG TCTCGGTGCT TCCAGCCACA TAACCACAAA ATCAATGGCT
(SEQ ID NO:49)     21bcon   AAAAAGAAGG TCTCGGTGCT TCCAGCCACA TAACCACAAA ATCAATGGCT
(SEQ ID NO:51)      29brc   AAAAAGAAGG TCTCGGTGCT TCCAGCCACA TAACCACAAA ATCAATGGCT

                              1613                                               1662
(SEQ ID NO:45)      Gdnfr   GCTCCTCCAA GCTGTGGTCT GAGCCCACTG CTGGTCCTGG TGGTAACCGC
(SEQ ID NO:54)     Hsgr-2   GCTCCTCCAA GCTGTGGTCT GAGCCCACTG CTGGTCCTGG TGGTAACCGC
(SEQ ID NO:55)     Hsgr-9   GCTCCTCCAA GCTGTGGTCT GAGCCCACTG CTGGTCCTGG TGGTAACCGC
(SEQ ID NO:52)  Hsgr-21ar   GCTCCTCCAA GCTGTGGTCT GAGCCCACTG CTGGTCCTGG TGGTAACCGC
(SEQ ID NO:53)  Hsgr-21br   GCTCCTCCAA GCTGTGGTCT GAGCCCACTG CTGGTCCTGG TGGTAACCGC
(SEQ ID NO:48)     21acon   GCTCCTCCAA GCTGTGGTCT GAGCCCACTG CTGGTCCTGG TGGTAACCGC
(SEQ ID NO:49)     21bcon   GCTCCTCCAA GCTGTGGTCT GAGCCCACTG CTGGTCCTGG TGGTAACCGC
(SEQ ID NO:51)      29brc   GCTCCTCCAA GCTGTGGTCT GAGCCCACTG CTGGTCCTGG TGGTAACCGC
```

FIG. 5M

```
                                1663                                            1712
(SEQ ID NO:45)      Gdnfr  TCTGTCCACC CTATTATCTT TAACAGAAAC ATCATAGCTG CATTAAAAAA
(SEQ ID NO:54)     Hsgr-2  TCTGTCCACC CTATTATCTT TAACAGAAAC ATCATAGCTG CATTAAAAAA
(SEQ ID NO:55)     Hsgr-9  TCTGTCCACC CTATTATCTT TAACAGAAAC ATCATAGCTG CATTAAAAAA
(SEQ ID NO:52)  Hsgr-21ar  TCTGTCCACC CTATTATCTT TAACAGAAA
(SEQ ID NO:53)  Hsgr-21br  TCTGTCCACC CTATTATCTT TAACAGAAA
(SEQ ID NO:48)     21acon  TCTGTCCACC CTATTATCTT TAACAGAAA
(SEQ ID NO:49)     21bcon  TCTGTCCACC CTATTATCTT TAACAGAAA
(SEQ ID NO:51)      29brc  TCTGTCCACC CTATTATCTT TAACAGAAAC ATCATAGCTG CATTAAAAAA

                                1713                                            1762
(SEQ ID NO:45)      Gdnfr  ATACAATATG GACATGTAAA AAGACAAAAA CCAAGTTATC TGTTTCCTGT
(SEQ ID NO:54)     Hsgr-2  ATACAATATG GACATGTAAA AAGACAAAAA CCAAGTTATC TGTTTCCTGT
(SEQ ID NO:55)     Hsgr-9  ATACAATATG GACATGTAAA AAGACAAAAA CCAAGTTATC TGTTTCCTGT
(SEQ ID NO:51)      29brc  ATACAATATG GACATGTAAA AAGACAAAAA CCAAGTTATC TGTTTCCTGT

                                1763                                            1812
(SEQ ID NO:45)      Gdnfr  TCTCTTGTAT AGCTGAAATT CCAGTTTAGG AGCTCAGTTG AGAAACAGTT
(SEQ ID NO:54)     Hsgr-2  TCTCTTGTAT AGCTGAAATT CCAGTTTAGG AGCTCAGTTG AGAAACAGTT
(SEQ ID NO:55)     Hsgr-9  TCTCTTGTAT AGCTGAAATT CCAGTTTAGG AGCTCAGTTG AGAAACAGTT
(SEQ ID NO:51)      29brc  TCTCTTGTAT AGCTGAAATT CCAGTTTAGG AGCTCAGTTG AGAAACAGTT

                                1813                                            1862
(SEQ ID NO:45)      Gdnfr  CCATTCAACT GGAACATTTT TTTTTTT.CC TTTTAAGAAA GCTTCTTGTG
(SEQ ID NO:54)     Hsgr-2  CCATTCAACT GGAACATTTT TTTTTTT.CC TTTTAAGAAA GCTTCTTGTG
(SEQ ID NO:55)     Hsgr-9  CCATTCAACT GGAACATTTT TTTTTTTTCC TTTTAAGAAA GCTTCTTGTG
(SEQ ID NO:51)      29brc  CCATTCAACT GGAACATTTT TTTTTTT.CC TTTTAAGAAA GCTTCTTGTG
```

FIG. 5N

```
                            1863                                             1912
(SEQ ID NO:45)      Gdnfr   ATCCTTcGGG GCTTCTGTGA AAAACCTGAT GCAGTGCTCC ATCCAAACTC
(SEQ ID NO:54)     Hsgr-2   ATCCTTCGGG GCTTCTGTGA AAAACCTGAT GCAGTGCTCC ATCCAAACTC
(SEQ ID NO:55)     Hsgr-9   ATCCTTTGGG GCTTCTGTGA AAAACCTGAT GCAGTGCTCC ATCCAAACTC
(SEQ ID NO:51)      29brc   ATCCTTCGGG GCTTCTGTGA AAAACCTGAT GCAGTGCTCC ATCCAAACTC

                            1913                                             1962
(SEQ ID NO:45)      Gdnfr   AGAAGGCTTT GGGATATGCT GTATTTTAAA GGGACAGTTT GTAACTTGGG
(SEQ ID NO:54)     Hsgr-2   AGAAGGCTTT GGGATATGCT GTATTTTAAA GGGACAGTTT GTAACTTGGG
(SEQ ID NO:55)     Hsgr-9   AGAAGGCTTT GGGATATGCT GTATTTTAAA GGGACAGTTT GTAACTTGGG
(SEQ ID NO:51)      29brc   AGAAGGCTTT GGGATATGCT GTATTTTAAA GGGACAGTTT GTAACTTGGG

                            1963                                             2012
(SEQ ID NO:45)      Gdnfr   CTGTAAAGCA AACTGGGGCT GTGTTTTCGA TGATGATGAT cATCATGATc
(SEQ ID NO:54)     Hsgr-2   CTGTAAAGCA AACTGGGGCT GTGTTTTCGA TGATGATGAT CATCATGATC
(SEQ ID NO:55)     Hsgr-9   CTGTAAAGCA AACTGGGGCT GTGTTTTCGA TGATGATGAT GATCATGATG
(SEQ ID NO:51)      29brc   CTGTAAAGCA AACTGGGGCT GTGTTTTCGA TGATGATGAT CATCATGATC

                            2013                                             2062
(SEQ ID NO:45)      Gdnfr   ATGAT..... .......... .......... .......... ....GATTTT
(SEQ ID NO:54)     Hsgr-2   ATGAT..... .......... .......... .......... ....GATTTT
(SEQ ID NO:55)     Hsgr-9   ATGATCATCA TGATCATGAT GATGATCATC ATGATCATGA TGATGATTTT
(SEQ ID NO:51)      29brc   ATGAT..... .......... .......... .......... ....GATTTT
```

FIG. 5O

```
                         2063                                         2112
(SEQ ID NO:45)   Gdnfr   AACAGTTTTA CTTCTGGCCT TTCCTAGCTA GAGAAGGAGT TAATATTTCT
(SEQ ID NO:54)  Hsgr-2   AACAGTTTTA CTTCTGGCCT TTCCTAGCTA GAGAAGGAGT TAATATTTCT
(SEQ ID NO:55)  Hsgr-9   AACAGTTTTA CTTCTGGCCT TTCCTAGCTA GAGAAGGAGT TAATATTTCT
(SEQ ID NO:51)   29brc   AACAGTTTTA CTTCTGGCCT TTCCTAGCTA GAGAAGGAGT TAATATTTCT

                         2113                                         2162
(SEQ ID NO:45)   Gdnfr   AAGGTAACTC CCATATCTCC TTTAATGACA TTGATTTCTA ATGATATAAA
(SEQ ID NO:54)  Hsgr-2   AAGGTAACTC CCATATCTCC TTTAATGACA TTGATTTCTA ATGATATAAA
(SEQ ID NO:55)  Hsgr-9   AAGGTAACTC CCATATCTCC TTTAATGACA TTGATTTCTA ATGATATAAA
(SEQ ID NO:51)   29brc   AAGGTAACTC CCATATCTCC TTTAATGACA TTGATTTCTA ATGATATAAA

                         2163                                         2212
(SEQ ID NO:45)   Gdnfr   TTTCAGCCTA CATTGATGCC AAGCTTTTTT GCCACAAAGA AGATTCTTAC
(SEQ ID NO:54)  Hsgr-2   TTTCAGCCTA CATTGATGCC AAGCTTTTTT GCCACAAAGA AGATTCTTAC
(SEQ ID NO:55)  Hsgr-9   TTTCAGCCTA CATTGATGCC AAGCTTTTTT GCCACAAAGA AGATTCTTAC
(SEQ ID NO:51)   29brc   TTTCAGCCTA CATTGATGCC AAGCTTTTTT GCCACAAAGA AGATTCTTAC

                         2213                                         2262
(SEQ ID NO:45)   Gdnfr   CAAGAGTGGG CTTTGTGGAA ACAGCTGGTA CTGATGTTCA CCTTTATATA
(SEQ ID NO:54)  Hsgr-2   CAAGAGTGGG CTTTGTGGAA ACAGCTGGTA CTGATGTTCA CCTTTATATA
(SEQ ID NO:55)  Hsgr-9   CAAGAGTGGG CTTTGTGGAA ACAGCTGGTA CTGATGTTCA CCTTTATATA
(SEQ ID NO:51)   29brc   CAAGAGTGGG CTTTGTGGAA ACAGCTGGTA CTGATGTTCA CCTTTATATA
```

FIG. 5P

```
                             2263                                                2312
(SEQ ID NO:45)       Gdnfr   TGTACTAGCA TTTTCCACGC TGATGTTTAT GTACTGTAAA CAGTTCTGCA
(SEQ ID NO:54)      Hsgr-2   TGTACTAGCA TTTTCCACGC TGATGTTTAT GTACTGTAAA CAGTTCTGCA
(SEQ ID NO:55)      Hsgr-9   TGTACTAGCA TTTTCCACGC TGATGTTTAT GTACTGTAAA CAGTTCTGCA
(SEQ ID NO:51)       29brc   TGTACTAGCA TTTTCCACGC TGATGTTTAT GTACTGTAAA CAGTTCTGCA

                             2313                                                2362
(SEQ ID NO:45)       Gdnfr   CTCTTGTACA AAAGAAAAAA CACCTGTCAC ATCCAAATAT AGTATCTGTC
(SEQ ID NO:54)      Hsgr-2   CTCTTGTACA AAAGAAAA
(SEQ ID NO:55)      Hsgr-9   CTCTTGTACA AAAGAAAA
(SEQ ID NO:51)       29brc   CTCTTGTACA AAAGAAAAAA CACCTGTCAC ATCCAAATAT AGTATCTGTC

                             2363                                                2412
(SEQ ID NO:45)       Gdnfr   TTTTCGTCAA AATAGAGAGT GGGGAATGAG TGTGCCGATT CAATACCTCA
(SEQ ID NO:51)       29brc   TTTTCGTCAA AATAGAGAGT GGGGAATGAG TGTGCCGATT CAATACCTCA

                             2413                                                2462
(SEQ ID NO:45)       Gdnfr   ATCCCTGAAC GACACTCTCC TAATCCTAAG CCTTACCTGA GTGAGAAGCC
(SEQ ID NO:51)       29brc   ATCCCTGAAC GACACTCTCC TAATCCTAAG CCTTACCTGA GTGAGAAGCC

                             2463                                                2512
(SEQ ID NO:45)       Gdnfr   CTTTACCTAA CAAAAGTCCA ATATAGCTGA AATGTCGCTC TAATACTCTT
(SEQ ID NO:51)       29brc   CTTTACCTAA CAAAAGTCCA ATATAGCTGA AATGTCGCTC TAATACTCTT

                             2513                                                2562
(SEQ ID NO:45)       Gdnfr   TACACATATG AGGTTATATG TAGAAAAAAA TTTTACTACT AAATGATTTC
(SEQ ID NO:51)       29brc   TACACATATG AGGTTATATG TAGAAAAAAA TTTTACTACT AAATGATTTC
```

FIG. 5Q

```
                                 2563                                            2612
(SEQ ID NO:45)        Gdnfr   AACTATTGGC TTTCTATATT TTGAAAGTAA TGATATTGTC TCATTTTTTT
(SEQ ID NO:51)        29brc   AACTATTGGC TTTCTATATT TTGAAAGTAA TGATATTGTC TCATTTTTTT

                                 2613                                            2662
(SEQ ID NO:45)        Gdnfr   ACTGATGGTT TAATACAAAA TACACAGAGC TTGTTTCCCC TCATAAGTAG
(SEQ ID NO:51)        29brc   ACTGATGGTT TAATACAAAA TACACAGAGC TTGTTTCCCC TCATAAGTAG

                                 2663                                            2712
(SEQ ID NO:45)        Gdnfr   TGTTCGCTCT GATATGAACT TCACAAATAC AGCTCATCAA AAGCAGACTC
(SEQ ID NO:51)        29brc   TGTTCGCTCT GATATGAACT TCACAAATAC AGCTCATCAA AAGCAGACTC

                                 2713                                            2762
(SEQ ID NO:45)        Gdnfr   TGAGAAGCCT CGTGCTGTAG CAGAAAGTTC TGCATCATGT GACTGTGGAC
(SEQ ID NO:51)        29brc   TGAGAAGCCT CGTGCTGTAG CAGAAAGTTC TGCATCATGT GACTGTGGAC

                                 2763                                            2812
(SEQ ID NO:45)        Gdnfr   AGGCAGGAGG AAACAGAACA GACAAGCATT GTCTTTTGTC ATTGCTCGAA
(SEQ ID NO:51)        29brc   AGGCAGGAGG AAACAGAACA GACAAGCATT GTCTTTTGTC ATTGCTCGAA

                                 2813                                            2862
(SEQ ID NO:45)        Gdnfr   GTGCAAGCGT GCATACCTGT GGAGGGAACT GGTGGCTGCT TGTAAATGTT
(SEQ ID NO:51)        29brc   GTGCAAGCGT GCATACCTGT GGAGGGAACT GGTGGCTGCT TGTAAATGTT

                                 2863                                            2912
(SEQ ID NO:45)        Gdnfr   CTGCAGCATC TCTTGACACA CTTGTCATGA CACAATCCAG TACCTTGGTT
(SEQ ID NO:51)        29brc   CTGCAGCATC TCTTGACACA CTTGTCATGA CACAATCCAG TACCTTGGTT
```

FIG. 5R

```
                             2913                                             2962
(SEQ ID NO:45)       Gdnfr   TTCAGGTTAT CTGACAAAGG CAGCTTTGAT TGGGACATGG AGGCATGGGC
(SEQ ID NO:51)       29brc   TTCAGGTTAT CTGACAAAGG CAGCTTTGAT TGGGACATGG AGGCATGGGC

                             2963
(SEQ ID NO:45)       Gdnfr   AGGCCGGAA
(SEQ ID NO:51)       29brc   AGGCCGGAA
```

FIG. 6

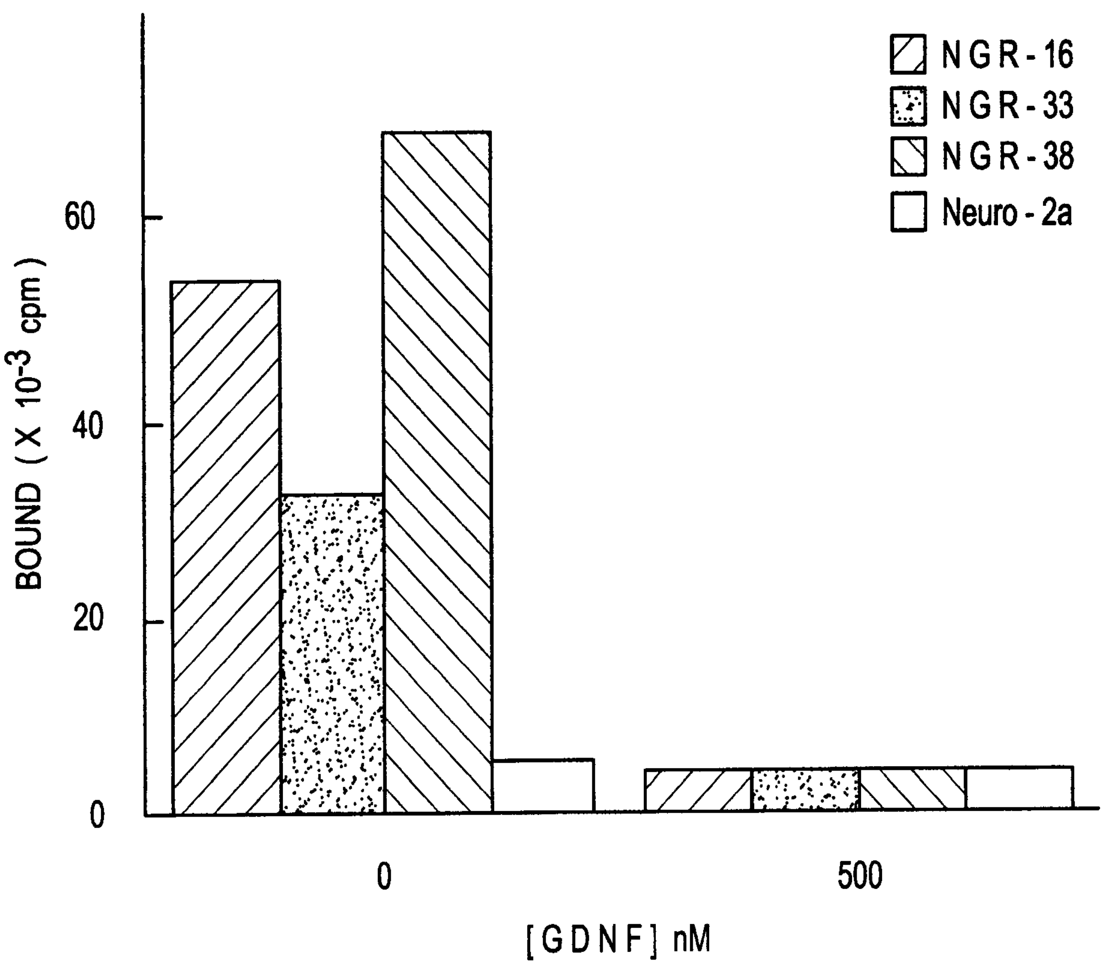

BOUND (X 10-3 cpm)
60
40
20
0
0
500
[G D N F] nM
N G R - 16
N G R - 33
N G R - 38
Neuro - 2a

FIG. 7A

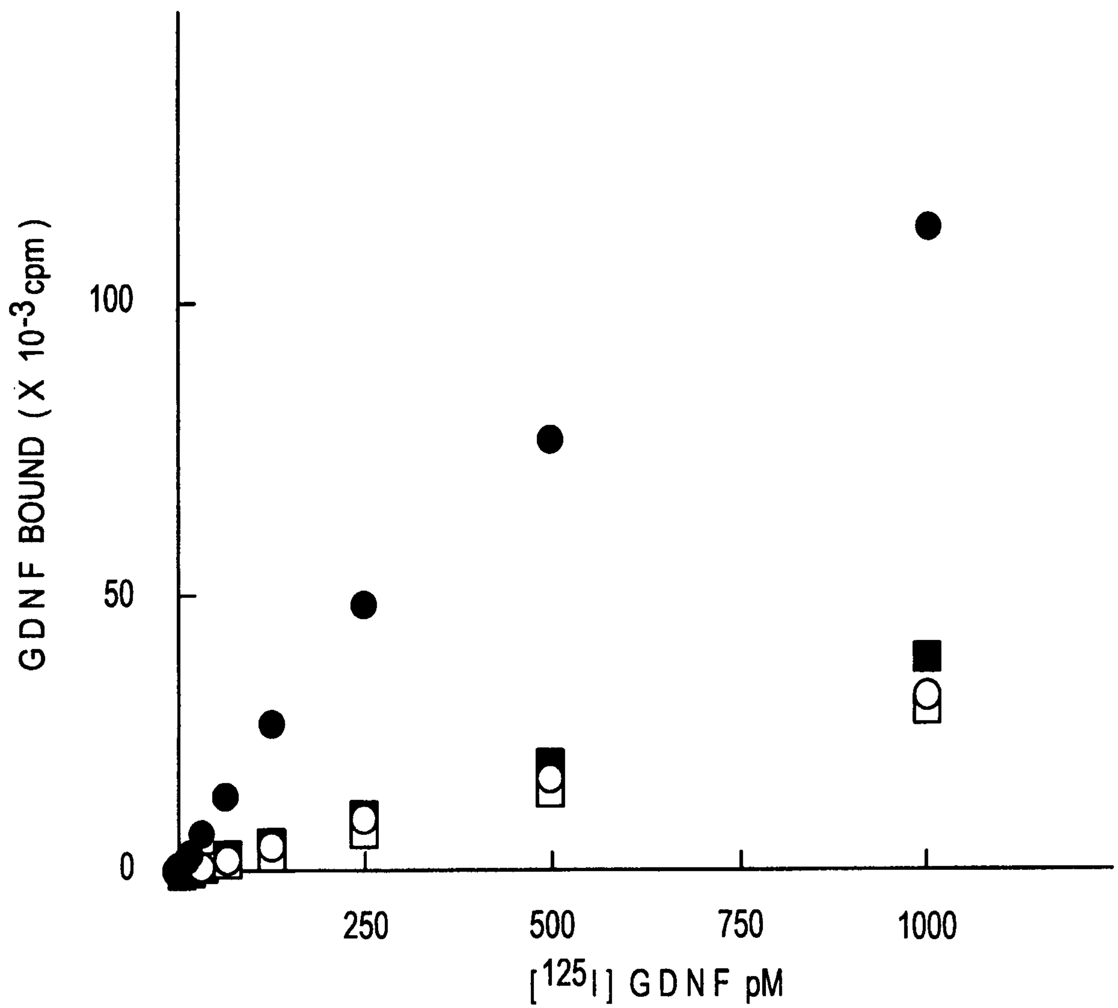


FIG. 7B

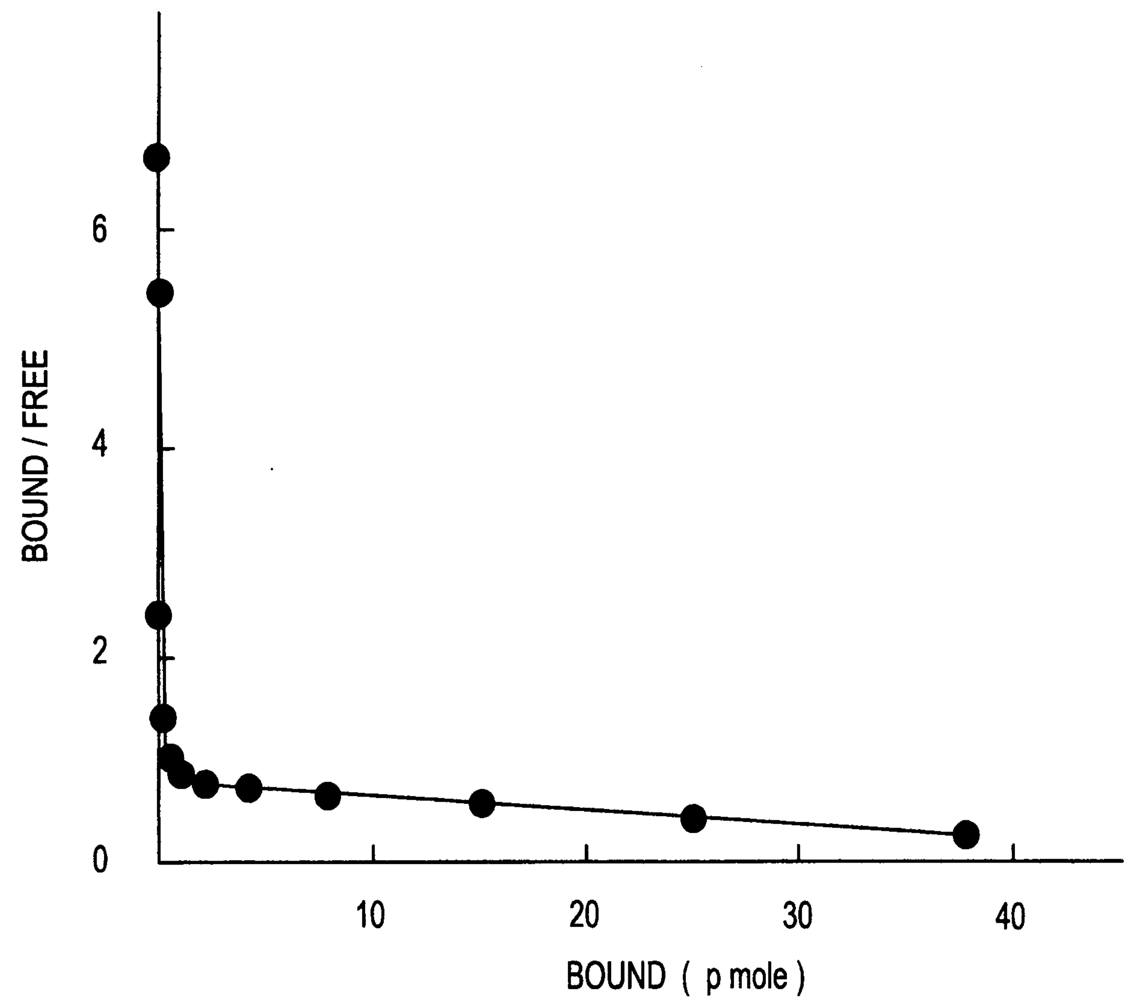


FIG.8

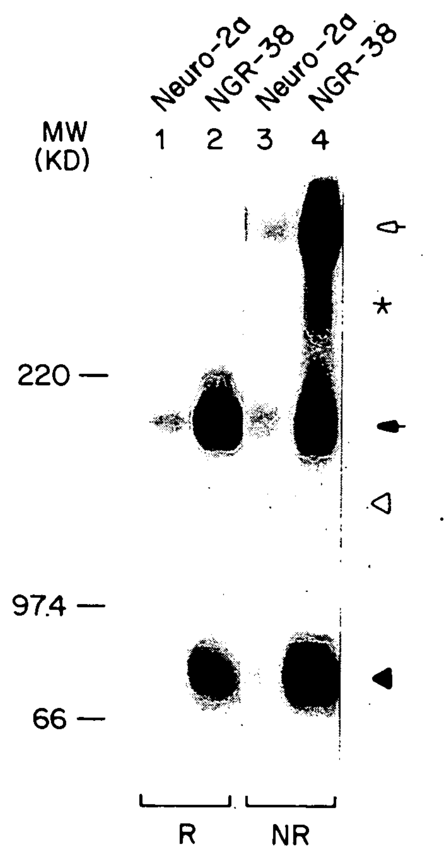
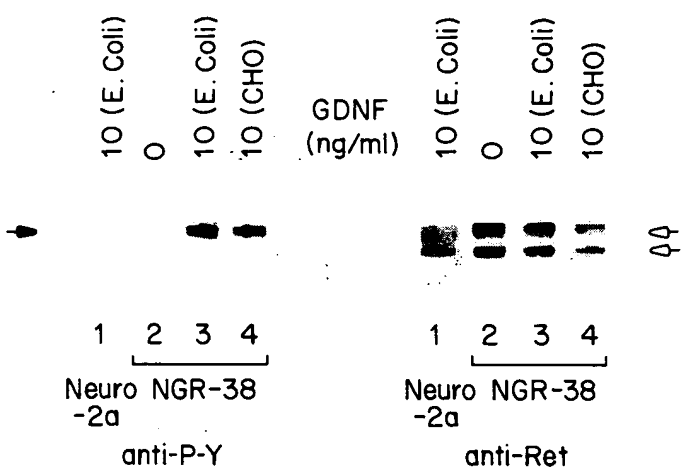


FIG.9A


10 (E. Coli)
0
10 (E. Coli)
10 (CHO)
GDNF (ng/ml)
10 (E. Coli)
0
10 (E. Coli)
10 (CHO)
1 2 3 4
Neuro -2a
NGR-38
anti-P-Y
1 2 3 4
Neuro -2a
NGR-38
anti-Ret

A

FIG.9B

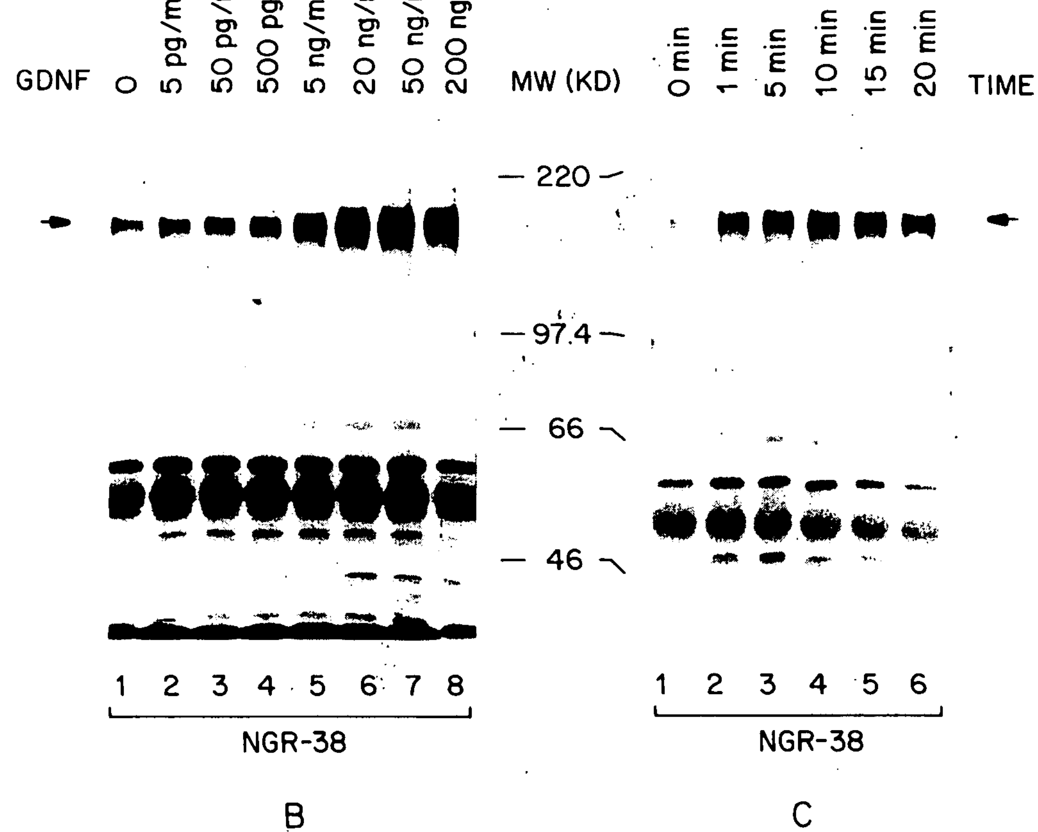

GDNF
0
5 pg/ml
50 pg/ml
500 pg/ml
5 ng/ml
20 ng/ml
50 ng/ml
200 ng/ml
MW (KD)
0 min
1 min
5 min
10 min
15 min
20 min
TIME
220
97.4
66
46
1 2 3 4 5 6 7 8
NGR-38
1 2 3 4 5 6
NGR-38
B
C

FIG. 10

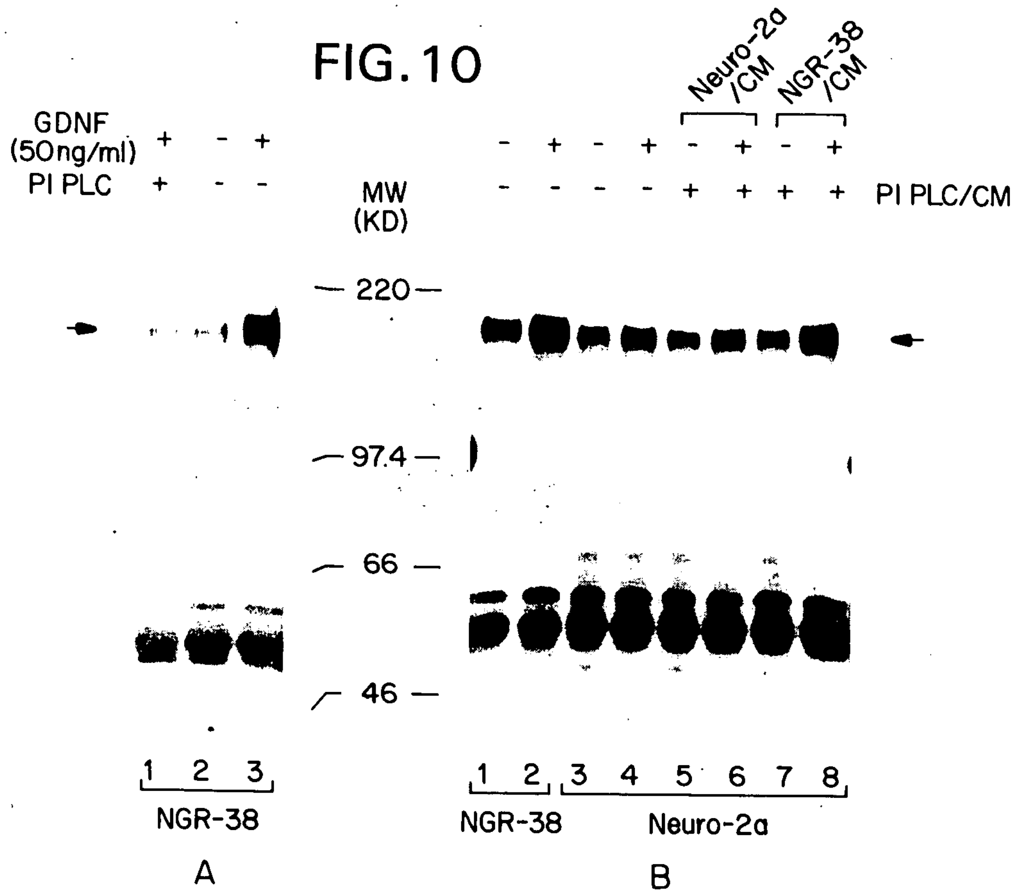

GDNF (50ng/ml)
PI PLC
MW (KD)
220
97.4
66
46
Neuro-2a /CM
NGR-38 /CM
PI PLC/CM
1 2 3
NGR-38
A
1 2 3 4 5 6 7 8
NGR-38
Neuro-2a
B

FIG. 11

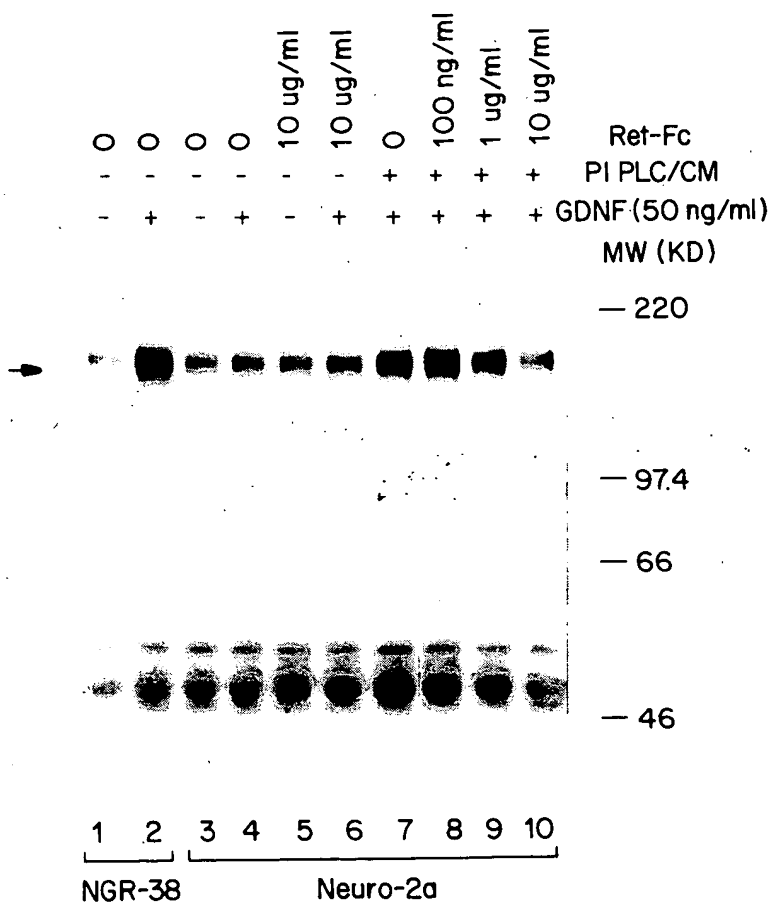

0
0
0
0
10 ug/ml
10 ug/ml
0
100 ng/ml
1 ug/ml
10 ug/ml
Ret-Fc
PI PLC/CM
GDNF (50 ng/ml)
MW (KD)
220
97.4
66
46
1 2 3 4 5 6 7 8 9 10
NGR-38
Neuro-2a

FIG.12

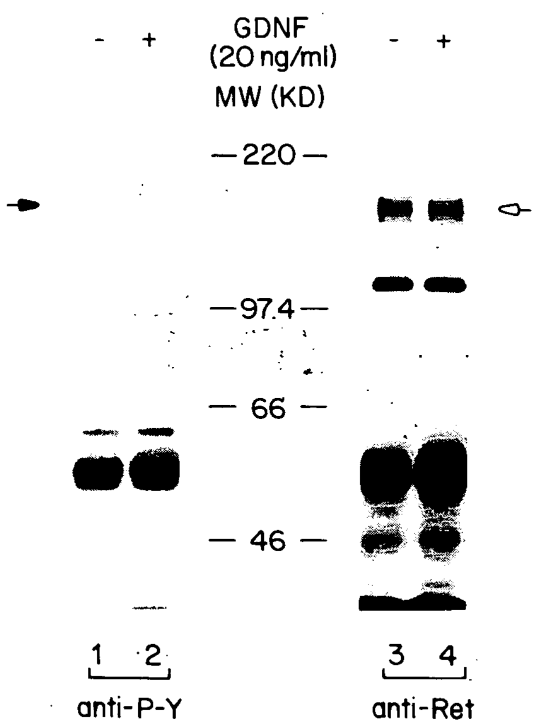


FIG. 13

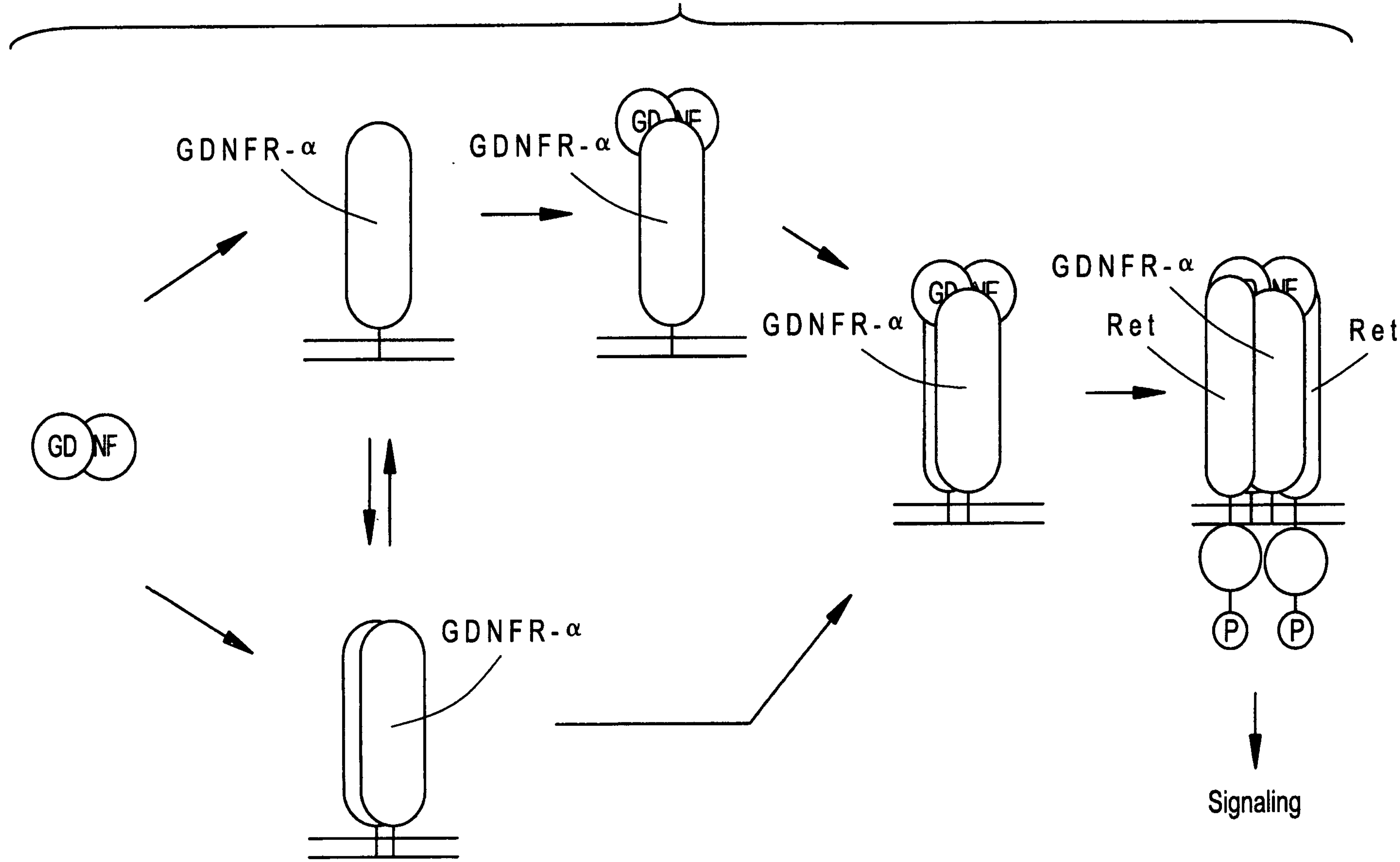

GD NF
GDNFR-α
GDNFR-α
GDNFR-α
GDNFR-α
GDNFR-α
Ret
Ret
P
P
Signaling

FIG.14A

Human GRR2

```
  1  CATGAAGAAACCTCAGTAAGTCTCAGACTTGGCCCAAAGGAGCCCAACTAGTTACTCCCT   60
 61  GGTCTGTTACAGAGGATCTGGCTATTACACTCAACAGCAAAAATTCAATTCAATCCCGCT  120
121  AAAGATATAAGAATCACTAGGAAKAATAAGCCAGAACTCAAGACAGAAATAGCATTAAGT  180
181  AGTTCCTTCAGTACAGTGAGCAGAAGCTGGCCACTCTACGACTCTAWAAGACTCAGAAAA  240
241  GCTTACTAGGGACCWCTGGGCATWCCGGTGTCCTATGTGGGATTTCGTAACGTCTTTGA   300
```

FIG.14B

301 GTCAGAAGCTGCCCTCAAAATAGTTTCTTCTCAAAACGGTTTCAGGCTTTGTTAGAAAGG 360

361 GAAGACTTCACTGCCACTTTACCCAGATCATCTACCCCATCCTTGGAATGAATGGGGAAG 420

421 CTTCAGCCACCCTACCAGGCTCCTAAAATCACCAACTTGAGAGAAAAACTATAACGTTGC 480

481 TCTACCAGTACTTCAGGAGGTTAAAGAAAGTCACAGAAGAAAAGAACTCTGGGGAAAACA 540

541 GTCAAATTCGGCTATTAAGACATTAGTTACAGGCCCCTGTACCTCTCCTCTAGAAACCCT 600

601 GGGAGTACACCCGCAGAGGAGAGAGAGCCCAAGCCACCAAGCAAAGTCAACCAATCTGGC 660

661 AAAGGGGCGTCCCACTGCGGCTTTCAGTCCAAGAAGTGGATCCTGCTGGTTCGCAGTCTC 720

FIG.14C

721	TCTTCTATCTCCTCACTTCCTATTTACCCTTTGAAGTGGGTACTGAATAGCCCGTTCCCA	780
781	AGCAGAGGCCCTTTGTATACGGGGTGCTACAGTCGCCTGGTGGAAACACCTTGGCAGAGT	840
841	TGTTTGGTGCCAGGATGGGCCACTGAAGGCATCTGCTGTGGACACACACACACACACACA	900
901	CACACACACACACACACACAGAGAGAGGAGAGAGAAAGACACACGCACGCAGAGACACAC	960
961	GGTCACTGGAATTCCATTAGAAAAAAGTGAGCCGAGCAAGGGTTAGCGGAGAAGATTTTT	1020
1021	TTTGAATCTTGTCTTCGTCTTGGTGCGAAAGAAGCGACTCCAGTCTCTCGTCCTCGAAGC	1080
1081	TCCGACTGGATTGTTCTTGGGCGCTGACACCCGTCTGTGGATTTCTTTTCTATTTGCATT	1140

FIG.14D

```
1141  TTATTCCGACCCCCTCCCTCGCCGCTTCCTTCCAGCCCTTCACTCGCAAATCGCCTCTCT  1200

1201  CCCCACCTCCCCAGGCCCCTCCTGGGAAGCGCAGGGGAATTGGACCCGCGGGGACTCACG  1260

1261  CCTTCCCGGACGATTGGAGGGGAGGGCTGACCCCAGGACTGGGCTGTTGGCTTAGAAAGC  1320

1321  CGATACACAGATACGCGTATATTTGATTGTAGCGGGCAAGGGGGCGTCGAGAGGCAGCA  1380

1381  GCCCATCGCCCGCCTCTCACCCCACCCCCTCCAGCCAGAGGCGAGAATCGCAGGACTCGG  1440

1441  GATCTTCATCGGGTGGACTAGCTGGGATCTCCGCATTGGATTTGGGGCTGATTACCACTG  1500
```

FIG.14E

```
1501   CTTGGCTATTATTATTGTTGTTGTTACTACTATTATTTTTTTTACCCAAGGGAGAAAGA   1560

1561   CAAAAAAACGGTGGGATTTATTTAACATGATCTTGGCAAACGTCTTCTGCCTCTTCTTCT  1620
   1                               M  I  L  A  N  V  F  C  L  F  F  F   12

1621   TTCTAGACGACACCCTCCGCTCTTTGGCCAGCCCTTCCTCCCTGCAGGGCCCCGAGCTCC  1680
  13    L  D  D  T  L  R  S  L  A  S  P  S  S  L  Q  G  P  E  L  H    32

1681   ACGGCTGGCGCCCCCCAGTGGACTGTGTCCGGGCCAATGAGCTGTGTGCCGCCGAATCCA  1740
  33    G  W  R  P  P  V  D  C  V  R  A  N  E  L  C  A  A  E  S  N    52

1741   ACTGCAGCTCTCGCTACCGCACTCTGCGGCAGTGCCTGGCAGGCCGCGACCGCAACACCA  1800
  53    C  S  S  R  Y  R  T  L  R  Q  C  L  A  G  R  D  R  N  T  M    72
```

FIG.14F

```
1801  TGCTGGCCAACAAGGAGTGCCAGGCGGCCTTGGAGGTCTTGCAGGAGAGCCCGCTGTACG  1860
  73   L  A  N  K  E  C  Q  A  A  L  E  V  L  Q  E  S  P  L  Y  D   92

1861  ACTGCCGCTGCAAGCGGGGCATGAAGAAGGAGCTGCAGTGTCTGCAGATCTACTGGAGCA  1920
  93   C  R  C  K  R  G  M  K  K  E  L  Q  C  L  Q  I  Y  W  S  I   112

1921  TCCACCTGGGGCTGACCGAGGGTGAGGAGTTCTACGAAGCCTCCCCCTATGAGCCGGTGA  1980
 113   H  L  G  L  T  E  G  E  E  F  Y  E  A  S  P  Y  E  P  V  T   132

1981  CCTCCCGCCTCTCGGACATCTTCAGGCTTGCTTCAATCTTCTCAGGGACAGGGGCAGACC  2040
 133   S  R  L  S  D  I  F  R  L  A  S  I  F  S  G  T  G  A  D  P   152

2041  CGGTGGTCAGCGCCAAGAGCAACCATTGCCTGGATGCTGCCAAGGCCTGCAACCTGAATG  2100
 153   V  V  S  A  K  S  N  H  C  L  D  A  A  K  A  C  N  L  N  D   172

2101  ACAACTGCAAGAAGCTGCGCTCCTCCTACATCTCCATCTGCAACCGCGAGATCTCGCCCA  2160
 173   N  C  K  K  L  R  S  S  Y  I  S  I  C  N  R  E  I  S  P  T   192
```

FIG.14G

```
2161  CCGAGCGCTGCAACCGCCGCAAGTGCCACAAGGCCCTGCGCCAGTTCTTCGACCGGGTGC  2220
 193    E  R  C  N  R  R  K  C  H  K  A  L  R  Q  F  F  D  R  V  P   212

2221  CCAGCGAGTACACCTACCGCATGCTCTTCTGCTCCTGCCAAGACCAGGCGTGCGCTGAGC  2280
 213    S  E  Y  T  Y  R  M  L  F  C  S  C  Q  D  Q  A  C  A  E  R   232

2281  GCCGCCGGCAAACCATCCTGCCCAGCTGCTCCTATGAGGACAAGGAGAAGCCCAACTGCC  2340
 233    R  R  Q  T  I  L  P  S  C  S  Y  E  D  K  E  K  P  N  C  L   252

2341  TGGACCTGCGTGGCGTGTGCCGGACTGACCACCTGTGTCGGTCCCGGCTGGCCGACTTCC  2400
 253    D  L  R  G  V  C  R  T  D  H  L  C  R  S  R  L  A  D  F  H   272

2401  ATGCCAATTGTCGAGCCTCCTACCAGACGGTCACCAGCTGCCCTGCGGACAATTACCAGG  2460
 273    A  N  C  R  A  S  Y  Q  T  V  T  S  C  P  A  D  N  Y  Q  A   292
```

FIG.14H

```
2461 CGTGTCTGGGCTCTTATGCTGGCATGATTGGGTTTGACATGACACCTAACTATGTGGACT 2520
293    C  L  G  S  Y  A  G  M  I  G  F  D  M  T  P  N  Y  V  D  S  312

2521 CCAGCCCCACTGGCATCGTGGTGTCCCCCTGGTGCAGCTGTCGTGGCAGCGGGAACATGG 2580
313    S  P  T  G  I  V  V  S  P  W  C  S  C  R  G  S  G  N  M  E  332

2581 AGGAGGAGTGTGAGAAGTTCCTCAGGGACTTCACCGAGAACCCATGCCTCCGGAACGCCA 2640
333    E  E  C  E  K  F  L  R  D  F  T  E  N  P  C  L  R  N  A  I  352

2641 TCCAGGCCTTTGGCAACGGCACGAACGTGAACGTGTCCCCAAAAGGCCCCTCGTTCCAGG 2700
353    Q  A  F  G  N  G  T  N  V  N  V  S  P  K  G  P  S  F  Q  A  372

2701 CCACCCAGGCCCCTCGGGTGGAGAAGACGCCTTCTTTGCCAGATGACCTCAGTGACAGTA 2760
373    T  Q  A  P  R  V  E  K  T  P  S  L  P  D  D  L  S  D  S  T  392
```

FIG.14I

```
2761  CCAGCTTGGGGACCAGTGTCATCACCACCTGCACGTCTGTCCAGGAGCAGGGGCTGAAGG  2820
393     S  L  G  T  S  V  I  T  T  C  T  S  V  Q  E  Q  G  L  K  A   412

2821  CCAACAACTCCAAAGAGTTAAGCATGTGCTTCACAGAGCTCACGACAAATATCATCCCAG  2880
413     N  N  S  K  E  L  S  M  C  F  T  E  L  T  T  N  I  I  P  G   432

2881  GGAGTAACAAGGTGATCAAACCTAACTCAGGCCCCAGCAGAGCCAGACCGTCGGCTGCCT  2940
433     S  N  K  V  I  K  P  N  S  G  P  S  R  A  R  P  S  A  A  L   452

2941  TGACCGTGCTGTCTGTCCTGATGCTGAAACTGGCCTTGTAGGCTGTGGGAACCGAGTCAG  3000
453     T  V  L  S  V  L  M  L  K  L  A  L  *                        464

3001  AAGATTTTTGAAAGCTACGCAGACAAGAACAGCCGCCTGACGAAATGGAAACACACACAG  3060
```

FIG.14J

3061 ACACACACACACCTTGCAAAAAAAAAATTGTTTTTCCCACCTTGTCGCTGAACCTGTCTC 3120

3121 CTCCCAGGTTTCTTCTCTGGAGAAGTTTTTGTAAACCAAACAGACAAGCAGGCAGGCAGC 3180

3181 CTGAGAGCTGGCCCAGGGGTCCCCTGGCAGGGAAACTCTGGTGCCGGGAGGCACGAG 3240

3241 GCTCTAGAAATGCCCTTCACTTTCTCCTGGTGTTTTTCTCTCTGGACCCTTCTGAAGCAG 3300

3301 AGACCGGACAAGAGCCTGCAGCGGAAGGGACTCTGGGCTGTGCCTGAGGCTGGCTGGGGG 3360

3361 CAGGACAACACAGCTGCTTCCCCAGGCTGCCCACTCTGGGGACCCGCTGGGGGCTGGCAG 3420

3421 AGGGCATCGGTCAGCGGGGCAGCGGGGCTGGCCATGAGGGTCCACCTTCAGCCCTTTGGC 3480

FIG.14K

3481	TTCAAGGATGGAGATGGTTTTGCCCTCCCTCTCTGCCCTCGGGTGGGCTGGTGGGTCTG	3540
3541	CAGCTGGTGTGGGAACTTCCCCACGGATGGCGGTGGAGGGGGTTCGCACCGTGCTGGGCT	3600
3601	CCCCCTGACTGTAGCACGGAGTGTTGGGGCTGGGGGCCAGCTCCAGGAGGGCTTGAGAGC	3660
3661	TCAGCCTGCCTGGGAGAGCCCTTGTGGCGAGGCATTAAAACTTGGGCACCAGCTTCTTTC	3720
3721	TCGGTGGCAGAAATTTTGAAGTCAGAGAGAAACGGTCCTTTGTTGGCTTCTTTGCTTTCT	3780
3781	CGTGGGTCCTTTGGCAGGCCTCCCTTTGGGGAGAGGGAGGGGAGAGACCACAGCCGGGTG	3840
3841	TGTGTCTGCAGCACCGTGGGCCCTCAAGCTTTCCTGCTGTCTTCTCCCTCCTCCTCCTTT	3900

FIG.14L

3901 CCCCTTTCTCTTTCCTCATTTCCTAGACGTACGTCAACTGTATGTACATACCGGGGCTCC 3960

3961 TCTCCTAACATATATGTATATACACATCCATATACATATATTGTGGTTTCCCCTTTCT 4020

4021 TTCCTTTTTTTAAGCAACAAAACTATGGAAATAATACCCCAACAGATGAGCGAAAATGTA 4080

4081 TTATTGTAAAGTTTATTTTTTTTAATACTGTTGTCTATAATGGGAAAAAGGACATTGGC 4140

4141 CCCGCAGTGCCCTGCCCCAGTCAGCCTGGCTGGGCTCTGGTGGGGGCTCCTGATCCGCAT 4200

4201 CCAAGCTTAACCAAGGCTCCAATAAACGTGCG 4232

FIG.15A

Human GRR3

```
1   CAAGTCAAAGGTTTAATCATGATCCAAGAGCCCAGAGAGACTTTAGGACAATAATAGGAA   60

61  TAAAGCAAGGCCCACAGGCTCCAGCTCCTGATGCCCAGATGTTCGGCAGGATCCGGGGAC  120

121 AGGGCAGTGCAGGCAGTAGTTTTCCATCCTCCATCCAGGGGAGGAGCGAGGGGAGCGCGG  180

181 AGCCCGGCGCCTACAGCTCGCCATGGTGCGCCCCCTGAACCCGCGACCGCTGCCGCCCGT  240
1                         M  V  R  P  L  N  P  R  P  L  P  P  V    13

241 AGTCCTGATGTTGCTGCTGCTGCTGCCGCCGTCGCCGCTGCCTCTCGCAGCCGGAGACCC  300
14   V  L  M  L  L  L  L  L  P  P  S  P  L  P  L  A  A  G  D  P    33
```

FIG.15B

```
                .         .         .         .         .         .
301  CCTTCCCACAGAAAGCCGACTCATGAACAGCTGTCTCCAGGCCAGGAGGAAGTGCCAGGC  360
 34   L  P  T  E  S  R  L  M  N  S  C  L  Q  A  R  R  K  C  Q  A    53

                .         .         .         .         .         .
361  TGATCCCACCTGCAGTGCTGCCTACCACCACCTGGATTCCTGCACCTCTAGCATAAGCAC  420
 54   D  P  T  C  S  A  A  Y  H  H  L  D  S  C  T  S  S  I  S  T    73

                .         .         .         .         .         .
421  CCCACTGCCCTCAGAGGAGCCTTCGGTCCCTGCTGACTGCCTGGAGGCAGCACAGCAACT  480
 74   P  L  P  S  E  E  P  S  V  P  A  D  C  L  E  A  A  Q  Q  L    93

                .         .         .         .         .         .
481  CAGGAACAGCTCTCTGATAGGCTGCATGTGCCACCGGCGCATGAAGAACCAGGTTGCCTG  540
 94   R  N  S  S  L  I  G  C  M  C  H  R  R  M  K  N  Q  V  A  C   113

                .         .         .         .         .         .
541  CTTGGACATCTATTGGACCGTTCACCGTGCCCGCAGCCTTGGTAACTATGAGCTGGATGT  600
114   L  D  I  Y  W  T  V  H  R  A  R  S  L  G  N  Y  E  L  D  V   133
```

FIG.15C

```
601  CTCCCCCTATGAAGACACAGTGACCAGCAAACCCTGGAAAATGAATCTCAGCAAACTGAA  660
134   S  P  Y  E  D  T  V  T  S  K  P  W  K  M  N  L  S  K  L  N   153

661  CATGCTCAAACCAGACTCAGACCTCTGCCTCAAGTTTGCCATGCTGTGTACTCTCAATGA  720
154   M  L  K  P  D  S  D  L  C  L  K  F  A  M  L  C  T  L  N  D   173

721  CAAGTGTGACCGGCTGCGCAAGGCCTACGGGGAGGCGTGCTCCGGGCCCCACTGCCAGCG  780
174   K  C  D  R  L  R  K  A  Y  G  E  A  C  S  G  P  H  C  Q  R   193

781  CCACGTCTGCCTCAGGCAGCTGCTCACTTTCTTCGAGAAGGCCGCCGAGCCCCACGCGCA  840
194   H  V  C  L  R  Q  L  L  T  F  F  E  K  A  A  E  P  H  A  Q   213

841  GGGCCTGCTACTGTGCCCATGTGCCCCCAACGACCGGGGCTGCGGGGAGCGCCGGCGCAA  900
214   G  L  L  L  C  P  C  A  P  N  D  R  G  C  G  E  R  R  R  N   233
```

FIG.15D

```
901   CACCATCGCCCCCAACTGCGCGCTGCCGCCTGTGGCCCCCAACTGCCTGGAGCTGCGGCG   960
234    T  I  A  P  N  C  A  L  P  P  V  A  P  N  C  L  E  L  R  R    253

961   CCTCTGCTTCTCCGACCCGCTTTGCAGATCACGCCTGGTGGATTTCCAGACCCACTGCCA   1020
254    L  C  F  S  D  P  L  C  R  S  R  L  V  D  F  Q  T  H  C  H    273

1021  TCCCATGGACATCCTAGGAACTTGTGCAACAGAGCAGTCCAGATGTCTACGAGCATACCT   1080
274    P  M  D  I  L  G  T  C  A  T  E  Q  S  R  C  L  R  A  Y  L    293

1081  GGGGCTGATTGGGACTGCCATGACCCCCAACTTTGCCAGCAATGTCAACACCAGTGTTGC   1140
294    G  L  I  G  T  A  M  T  P  N  F  A  S  N  V  N  T  S  V  A    313

1141  CTTAAGCTGCACCTGCCGAGGCAGTGGCAACCTGCAGGAGGAGTGTGAAATGCTGGAAGG   1200
314    L  S  C  T  C  R  G  S  G  N  L  Q  E  E  C  E  M  L  E  G    333
```

FIG.15E

```
              .         .         .         .         .         .
1201  GTTCTTCTCCCACAACCCCTGCCTCACGGAGGCCATTGCAGCTAAGATGCGTTTTCACAG  1260
 334   F  F  S  H  N  P  C  L  T  E  A  I  A  A  K  M  R  F  H  S   353

              .         .         .         .         .         .
1261  CCAACTCTTCTCCCAGGACTGGCCACACCCTACCTTTGCTGTGATGGCACACCAGAATGA  1320
 354   Q  L  F  S  Q  D  W  P  H  P  T  F  A  V  M  A  H  Q  N  E   373

              .         .         .         .         .         .
1321  AAACCCTGCTGTGAGGCCACAGCCCTGGGTGCCCTCTCTTTTCTCCTGCACGCTTCCCTT  1380
 374   N  P  A  V  R  P  Q  P  W  V  P  S  L  F  S  C  T  L  P  L   393

              .         .         .         .         .         .
1381  GATTCTGCTCCTGAGCCTATGGTAGCTGGACTTCCCCAGGGCCCTCTTCCCCTCCACCAC  1440
 394   I  L  L  L  S  L  W  *                                       400

              .         .         .         .         .         .
1441  ACCCAGGTGGACTTGCAGCCCACAAGGGGTGAGGAAAGGACAGCAGCAGGAAGGAGGTGC  1500
```

FIG.15F

```
1501  AGTGCGCAGATGAGGGCACAGGAGAAGCTAAGGGTTATGACCTCCAGATCCTTACTGGTC  1560

1561  CAGTCCTCATTCCCTCCACCCCATCTCCACTTCTGATTCATGCTGCCCCTCCTTGGTGGC  1620

1621  CACAATTTAGCCATGTCATCTGGTGGTGACCAGCTCCACCAAGCCCCTTTGTGAGCCCTT  1680

1681  CCTCTTGACTACCAGGATCACCAGAATCTAATAAGTTAGCCTTTCTCTATTGCATTCCAG  1740

1741  ATTAGGGTTAGGGTAGGGAGGACTGGGTGTTCTGAGGCAGCCTAGAAAGTCATTCTCCTT  1800

1801  TGTGAAGAAGGCTCCTGCCCCCTCGTCTCCTCCTCTGAGTGGAGGATGGAAAACTACTGC  1860

1861  CTGCACTGCCCTGTCCCCGGATCCTGCCGAACATCTGGGCATCAGGAGCTGGAGCCTGTG  1920
```

FIG.15G

```
1921  GGCCTTGCTTTATTCCTATTATTGTCCTAAAGTCTCTCTGGGCTCTTGGATCATGATTAA  1980

1981  ACCTTTGACTG  1991
```

FIG.16A

Rat GRR2

```
  1  GCGGCCGCGTCGACCTTGACCATGCAGACACTTTTTCAGGCCTCTGTCTGGTGTGAAGTT   60
 61  GGCAGATACAAGCAAGGCCCGAAAGGGGTCTCAGCTTCTCTCCTGGGCCTCCTGGACT   120
121  GAGTTAGGCTTGCTTCTGGTTGTCTTCTAAAGGCACGGTGATACAGAATGATGAGACTAG   180
181  GCTGGAGGGGGCTTTCTGCTTCTCTGTGTGTGACCTTGAGTTATCTCCCTTCGTTGGATC   240
241  CGAGCTTTCCTGGAATATGATGTTGAATATGAATATGAGTTCTGCCTAAGGTCCAGACAG   300
```

FIG.16B

```
301   GCTCTGAGGGTTAACTGACTTTTGGAGCCTTCAAATCAATACCTTGGATGGAGTGGGGT   360

361   TTGTCCAATGGGAGTTGAGGCAAGATCCCTTTGCATAAGCCTTGCCACATCATGTTGAAG   420

421   CCATGCCATTCTGTCTGGACTATTGGCATCTTACCTTTCCAGCAGTTTCAGTGAAGGCCT   480

481   TCCTGGATTTATCATTCTGTGTTCCACTGCCTAGGATTGTGCTCAAGAGGAAATGAATGT   540

541   GAACCATGGTTGTAGGGGAGTATGGCCAACCAGGTTGGGTCTGTGTTGACCTTGGTCTTG   600
  1         M  V  V  G  E  Y  G  Q  P  G  W  V  C  V  D  L  G  L  G    19

601   GTGTTCTTTTGTGTAAAGTGGGTGAGAAGTTCCTTCAAACCTTAGGCCTACATTGGGGTC   660
 20    V  L  L  C  K  V  G  E  K  F  L  Q  T  L  G  L  H  W  G  Q    39
```

FIG.16C

```
661  AGAGACTGTGGTGGCCCTCATTCATGCTTGTCTTCCCTTCCCACTACCCAGACGAAACCC  720
 40    R  L  W  W  P  S  F  M  L  V  F  P  S  H  Y  P  D  E  T  L   59

721  TCCGCTCTTTGGCCAGCCCTTCCTCCCTGCAGGGCTCTGAGCTCCACGGCTGGCGCCCCC  780
 60    R  S  L  A  S  P  S  S  L  Q  G  S  E  L  H  G  W  R  P  Q   79

781  AAGTGGACTGTGTCCGGGCCAATGAGCTGTGTGCGGCTGAATCCAACTGCAGCTCCAGGT  840
 80    V  D  C  V  R  A  N  E  L  C  A  A  E  S  N  C  S  S  R  Y   99

841  ACCGCACCCTTCGGCAGTGCCTGGCAGGCCGGGATCGCAATACCATGCTGGCCAATAAGG  900
100    R  T  L  R  Q  C  L  A  G  R  D  R  N  T  M  L  A  N  K  E  119

901  AGTGCCAGGCAGCCCTGGAGGTCTTGCAGGAAAGCCCACTGTATGACTGCCGCTGCAAGC  960
120    C  Q  A  A  L  E  V  L  Q  E  S  P  L  Y  D  C  R  C  K  R  139
```

FIG.16D

```
961   GGGGCATGAAGAAGGAGCTGCAGTGTCTGCAGATCTACTGGAGCATCCATCTGGGGCTGA   1020
140    G  M  K  K  E  L  Q  C  L  Q  I  Y  W  S  I  H  L  G  L  T    159

1021  CAGAGGGTGAGGAGTTCTATGAAGCTTCCCCCTATGAGCCTGTGACCTCGCGCCTCTCGG   1080
160    E  G  E  E  F  Y  E  A  S  P  Y  E  P  V  T  S  R  L  S  D    179

1081  ACATCTTCAGGCTCGCTTCAATCTTCTCAGGGACAGGGACAGACCCGGCGGTCAGTACCA   1140
180    I  F  R  L  A  S  I  F  S  G  T  G  T  D  P  A  V  S  T  K    199

1141  AAAGCAACCACTGCCTGGATGCCGCCAAGGCCTGCAACCTGAATGACAACTGCAAGAAGC   1200
200    S  N  H  C  L  D  A  A  K  A  C  N  L  N  D  N  C  K  K  L    219

1201  TTCGCTCCTCTTATATCTCCATCTGCAACCGTGAGATCTCTCCCACCGAACGCTGCAACC   1260
220    R  S  S  Y  I  S  I  C  N  R  E  I  S  P  T  E  R  C  N  R    239
```

FIG.16E

```
1261  GCCGCAAGTGCCACAAGGCTCTGCGCCAGTTCTTTGACCGTGTGCCCAGCGAGTATACCT  1320
 240    R  K  C  H  K  A  L  R  Q  F  F  D  R  V  P  S  E  Y  T  Y   259

1321  ACCGCATGCTCTTCTGCTCCTGTCAGGACCAGGCATGTGCTGAGCGTCGCCGGCAAACCA  1380
 260    R  M  L  F  C  S  C  Q  D  Q  A  C  A  E  R  R  R  Q  T  I   279

1381  TCCTGCCCAGTTGCTCCTATGAGGACAAGGAGAAGCCCAACTGCCTGGACCTGCGCAGCC  1440
 280    L  P  S  C  S  Y  E  D  K  E  K  P  N  C  L  D  L  R  S  L   299

1441  TGTGTCGTACAGACCACCTGTGCCGGTCCCGACTGGCAGATTTCCACGCCAACTGTCGAG  1500
 300    C  R  T  D  H  L  C  R  S  R  L  A  D  F  H  A  N  C  R  A   319

1501  CCTCCTACCGGACAATCACCAGCTGTCCTGCGGACAACTACCAGGCATGTCTGGGCTCCT  1560
 320    S  Y  R  T  I  T  S  C  P  A  D  N  Y  Q  A  C  L  G  S  Y   339
```

FIG.16F

```
1561  ATGCTGGCATGATTGGGTTTGATATGACACCCAACTATGTGGACTCCAACCCCACGGGCA  1620
340    A  G  M  I  G  F  D  M  T  P  N  Y  V  D  S  N  P  T  G  I   359

1621  TCGTGGTGTCTCCCTGGTGCAATTGTCGTGGCAGTGGGAACATGGAAGAAGAGTGTGAGA  1680
360    V  V  S  P  W  C  N  C  R  G  S  G  N  M  E  E  E  C  E  K   379

1681  AGTTCCTCAGGGACTTCACGGAAAACCCATGCCTCCGGAATGCCATTCAGGCCTTTGGTA  1740
380    F  L  R  D  F  T  E  N  P  C  L  R  N  A  I  Q  A  F  G  N   399

1741  ATGGCACAGATGTGAACATGTCTCCCAAAGGCCCCTCACTCCCAGCTACCCAGGCCCCTC  1800
400    G  T  D  V  N  M  S  P  K  G  P  S  L  P  A  T  Q  A  P  R   419

1801  GGGTGGAGAAGACTCCTTCACTGCCAGATGACCTCAGTGACAGCACCAGCCTGGGGACCA  1860
420    V  E  K  T  P  S  L  P  D  D  L  S  D  S  T  S  L  G  T  S   439

1861  GTGTCATCACCACCTGCACATCTATCCAGGAGCAAGGGCTGAAGGCCAACAACTCCAAAG  1920
```

FIG.16G

```
440   V I T T C T S I Q E Q G L K A N N S K E   459

           .         .         .         .         .         .
1921  AGTTAAGCATGTGCTTCACAGAGCTCACGACAAACATCAGTCCAGGGAGTAAAAAGGTGA  1980
460   L S M C F T E L T T N I S P G S K K V I   479

           .         .         .         .         .         .
1981  TCAAACTTAACTCAGGCTCCAGCAGAGCCAGACTGTCGGCTGCCTTGACTGCCCTCCCAC  2040
480   K L N S G S S R A R L S A A L T A L P L   499

           .         .         .         .         .         .
2041  TCCTGATGCTGACCTTGGCCTTGTAGGCCTTTGGAACCCAGCACAAAAGTTCTTCAAGCA  2100
500   L M L T L A L *                           506

           .         .         .         .         .         .
2101  ACCCAGATATGAACTCCCGCCTGACAAAATGGAAACACACGCATACACACATGCCACACA  2160

           .         .         .         .         .
2161  CAGACACACACACAGACACACACACACACACATACAGACGTCGACGCGGCCGC  2215
```

FIG.17A

Rat GRR3

```
                 .         .         .         .         .         .
  1  GCGGCCGCGTCGACCGACGCCCAGCACAGGCAGAGCGCTGCCGGGTCCGCGGCGTCCAGA   60

                 .         .         .         .         .         .
 61  CCCGCCATGGGGCTCTCCCGGAGCCCGCGACCGCCGCCGCTAGTGATCCTGCTACTGGTG  120
  1        M  G  L  S  R  S  P  R  P  P  P  L  V  I  L  L  L  V    18

                 .         .         .         .         .         .
121  CTGTCGCTGTGGCTACCCCTTGGAACAGGAAACTCCCTTCCCACAGAGAACAGGCTTGTG  180
 19  L  S  L  W  L  P  L  G  T  G  N  S  L  P  T  E  N  R  L  V    38

                 .         .         .         .         .         .
181  AACAGCTGTACCCAGGCCAGAAAAAAATGCGAGGCTAATCCCGCTTGCAAGGCTGCCTAC  240
 39  N  S  C  T  Q  A  R  K  K  C  E  A  N  P  A  C  K  A  A  Y    58
```

FIG.17B

```
                 .         .         .         .         .         .
241   CAGCACCTGGACTCCTGCACCCCCAGTCTCAGCAGTCCACTGCCCTCAGGGGAGTCTGCC   300
 59   Q  H  L  D  S  C  T  P  S  L  S  S  P  L  P  S  G  E  S  A     78

                 .         .         .         .         .         .
301   ACATCTGCAGCGTGCCTTGAAGCAGCACAGCAACTCAGGAACAGCTCTCTCATAGACTGC   360
 79   T  S  A  A  C  L  E  A  A  Q  Q  L  R  N  S  S  L  I  D  C     98

                 .         .         .         .         .         .
361   AGGTGCCACCGGCGCATGAAGCACCAAGCTACCTGTCTGGACATTTATTGGACCGTTCAC   420
 99   R  C  H  R  R  M  K  H  Q  A  T  C  L  D  I  Y  W  T  V  H     118

                 .         .         .         .         .         .
421   CCTGTCCGAAGCCTTGGTGACTACGAGTTGGACGTCTCACCCTATGAAGACACAGTGACC   480
119   P  V  R  S  L  G  D  Y  E  L  D  V  S  P  Y  E  D  T  V  T     138

                 .         .         .         .         .         .
481   AGCAAACCCTGGAAAATGAATCTCAGCAAGCTGAGCATGCTCAAACCAGACTCCGACCTC   540
139   S  K  P  W  K  M  N  L  S  K  L  S  M  L  K  P  D  S  D  L     158
```

FIG.17C

```
541  TGCCTCAAATTTGCTATGCTGTGTACTCTTAACGACAAGTGCGACCGCCTCCGAAAGGCC  600
159  C  L  K  F  A  M  L  C  T  L  N  D  K  C  D  R  L  R  K  A    178

601  TACGGGGAGGCGTGCTCAGGGATCCGCTGCCAGCGCCACCTCTGCCTAGCTCAGCTGCGC  660
179  Y  G  E  A  C  S  G  I  R  C  Q  R  H  L  C  L  A  Q  L  R    198

661  TCCTTCTTCGAGAAGGCGGCAGAGTCCCACGCTCAGGGCCTGCTGCTGTGTCCCTGTGCA  720
199  S  F  F  E  K  A  A  E  S  H  A  Q  G  L  L  L  C  P  C  A    218

721  CCCGAAGATGCGGGCTGTGGGGAGCGCCGGCGCAACACCATCGCCCCCAGTTGCGCCCTC  780
219  P  E  D  A  G  C  G  E  R  R  R  N  T  I  A  P  S  C  A  L    238

781  CCGTCTGTGGCCCCCAACTGCCTAGATCTTCGGAGCTTCTGCCGTGCGGACCCTCTGTGC  840
239  P  S  V  A  P  N  C  L  D  L  R  S  F  C  R  A  D  P  L  C    258
```

FIG.17D

```
841  AGATCACGCCTGATGGACTTCCAGACCCACTGCCACCCTATGGACATCCTCGGGACTTGT  900
259  R  S  R  L  M  D  F  Q  T  H  C  H  P  M  D  I  L  G  T  C   278

901  GCAACTGAGCAGTCCAGATGTCTGCGGGCATACCTGGGGCTAATTGGGACTGCCATGACC  960
279  A  T  E  Q  S  R  C  L  R  A  Y  L  G  L  I  G  T  A  M  T   298

961  CCAAACTTCATCAGCAAGGTCAACACTACTGTTGCCTTAGGCTGTACCTGCCGAGGCAGT  1020
299  P  N  F  I  S  K  V  N  T  T  V  A  L  G  C  T  C  R  G  S   318

1021 GGCAACCTGCAGGACGAGTGTGAACAGCTGGAAAAGTCCTTCTCCCAGAACCCCTGCCTC  1080
319  G  N  L  Q  D  E  C  E  Q  L  E  K  S  F  S  Q  N  P  C  L   338

1081 ATGGAGGCCATTGCGGCTAAAATGCGTTTCCACAGACAACTCTTCTCCCAGGACTGGGCG  1140
339  M  E  A  I  A  A  K  M  R  F  H  R  Q  L  F  S  Q  D  W  A   358
```

FIG.17E

```
                .         .         .         .         .         .
1141 GACTCTACTTTTTCTGTGATGCAGCAGCAGAACAGCAGCCCTGCTCTGAGGCCCCAGCTC 1200
 359 D  S  T  F  S  V  M  Q  Q  Q  N  S  S  P  A  L  R  P  Q  L   378

                .         .         .         .         .         .
1201 AGGCTACCCGTTCTGTCTTTCTTCATCCTTACCTTGATTCTGCTGCAGACCCTCTGGTAA 1260
 379 R  L  P  V  L  S  F  F  I  L  T  L  I  L  L  Q  T  L  W  *   397

                .         .         .         .         .         .
1261 CTGGGCTCCCTCAGGGTCCTTTGTCCTCTCCACCACACCCAGACCGACTTGCAGCCTGTG 1320

                .         .         .         .         .         .
1321 ATGGGAGAGAAAATGCTGGCCTCTGGAAGAAGATGCAACCAGGCTCACTGCACATCCTGT 1380

                .         .         .         .         .         .
1381 CTGCTCCAGATGAGGTCTTGGAAGAAGCGAGGGCTGTGACCGTTCAGAATCCTGAGCGGC 1440

                .         .         .         .         .         .
1441 CAGCTTTCAAACCTCTCCTACTTACTCCTGCTTGGGCTGCTCCTCCCTAGGACCTTGTAC 1500
```

FIG.17F

```
1501  TCCAGTTTGGCTGTATATTGTGGTGGTGATTAGCTTCCCACCTCCAGCCCTTCTTCCTGT  1560

1561  TTCCCAGGACCACCCAGGGCTAATGACTCACTCATTCCTGGTTGCCTTCTCCAGGAAGGC  1620

1621  AGGCTGAGGGTTCTGAGGCAGCTGAGAAAGATGGTCCCTTTGTGAGGAAGGCTGGTGGTC  1680

1681  CAACCGTCGACGCGGCCGC  1699
```

FIG.18A

Alignment of the Amino Acid Sequeces of GDNFRs

```
         1                                                         50
Mgdnfr   ~~~~~~~~~~ ~~~~MFLATL YFVLPLLDLL MSAEVSG.GD RLDCVKASDQ
Rgdnfr   ~~~~~~~~~~ ~~~~MFLATL YFALPLLDLL MSAEVSG.GD RLDCVKASDQ
Hgdnfr   ~~~~~~~~~~ ~~~~MFLATL YFALPLLDLL LSAEVSG.GD RLDCVKASDQ
 Hgrr2   ~~~~MILANV FCLFFFLDDT LRSLASPSSL QGPELHGWRP PVDCVRANEL
 Rgrr2   ~~~~~~~~ML VFPSHYPDET LRSLASPSSL QGSELHGWRP QVDCVRANEL
 Hgrr3   MVRPLNPRPL PPVVLMLLLL LPPSPLPLAA GDPLPTESRL MNSCLQARRK
 Rgrr3   MGLSRSPRPP PLVILLLVLS L...WLPLGT GNSLPTENRL VNSCTQARKK
```

FIG.18B

```
          51                                                100
Mgdnfr    CLKEQSCSTK YRTLRQCVAG KETNFSLTSG LEAKDECRSA MEALKQKSLY
Rgdnfr    CLKEQSCSTK YRTLRQCVAG KETNFSLTSG LEAKDECRSA MEALKQKSLY
Hgdnfr    CLKEQSCSTK YRTLRQCVAG KETNFSLASG LEAKDECRSA MEALKQKSLY
 Hgrr2    CAAESNCSSR YRTLRQCLAG RDRNTML... ..ANKECQAA LEVLQESPLY
 Rgrr2    CAAESNCSSR YRTLRQCLAG RDRNTML... ..ANKECQAA LEVLQESPLY
 Hgrr3    CQADPTCSAA YHHLDSCTSS ISTPLP.SEE PSVPADCLEA AQQLRNSSLI
 Rgrr3    CEANPACKAA YQHLDSCTPS LSSPLP.SGE SATSAACLEA AQQLRNSSLI
```

FIG.18C

```
        101                                                    150
Mgdnfr  NCRCKRGMKK EKNCLRIYWS MYQSL.QGND LLEDSPYEPV NSRLSDIFRA
Rgdnfr  NCRCKRGMKK EKNCLRIYWS MYQSL.QGND LLEDSPYEPV NSRLSDIFRA
Hgdnfr  NCRCKRGMKK EKNCLRIYWS MYQSL.QGND LLEDSPYEPV NSRLSDIFRV
 Hgrr2  DCRCKRGMKK ELQCLQIYWS IHLGLTEGEE FYEASPYEPV TSRLSDIFRL
 Rgrr2  DCRCKRGMKK ELQCLQIYWS IHLGLTEGEE FYEASPYEPV TSRLSDIFRL
 Hgrr3  GCMCHRRMKN QVACLDIYWT VHRARSLGNY ELDVSPYE.. .....DTVTS
 Rgrr3  DCRCHRRMKH QATCLDIYWT VHPVRSLGDY ELDVSPYE.. .....DTVTS
```

FIG.18D

```
        151                                                   200
Mgdnfr  VPFISDVFQQ VEHISKGNNC LDAAKACNLD DTCKKYRSAY ITPCTTSMS.
Rgdnfr  VPFISDVFQQ VEHISKGNNC LDAAKACNLD DTCKKYRSAY ITPCTTSMS.
Hgdnfr  VPFISDVFQQ VEHIPKGNNC LDAAKACNLD DICKKYRSAY ITPCTTSVS.
 Hgrr2  ASIFSGTGAD PVVSAKSNHC LDAAKACNLN DNCKKLRSSY ISICNREISP
 Rgrr2  ASIFSGTGTD PAVSTKSNHC LDAAKACNLN DNCKKLRSSY ISICNREISP
 Hgrr3  KPWKMNLSKL NMLKPDSDLC LKFAMLCTLN DKCDRLRKAY GEACS.....
```

FIG.18E

```
Rgrr3   KPWKMNLSKL SMLKPDSDLC LKFAMLCTLN DKCDRLRKAY GEACS.....

        201                                               250
Mgdnfr  NEVCNRRKCH KALRQFFDKV PAKHSYGMLF CSC..RDVAC TERRRQTIVP
Rgdnfr  NEVCNRRKCH KALRQFFDKV PAKHSYGMLF CSC..RDIAC TERRRQTIVP
Hgdnfr  NDVCNRRKCH KALRQFFDKV PAKHSYGMLF CSC..RDIAC TERRRQTIVP
 Hgrr2  TERCNRRKCH KALRQFFDRV PSEYTYRMLF CSC..QDQAC AERRRQTILP
 Rgrr2  TERCNRRKCH KALRQFFDRV PSEYTYRMLF CSC..QDQAC AERRRQTILP
 Hgrr3  GPHCQRHVCL RQLLTFFEKA AEPHAQGLLL CPCAPNDRGC GERRRNTIAP
 Rgrr3  GIRCQRHLCL AQLRSFFEKA AESHAQGLLL CPCAPEDAGC GERRRNTIAP
```

FIG.18F

	251				300
Mgdnfr	VCSYEERERP	NCLNLQDSCK	TNYICRSRLA	DFFTNCQPES	RSVSNCLKEN
Rgdnfr	VCSYEERERP	NCLSLQDSCK	TNYICRSRLA	DFFTNCQPES	RSVSNCLKEN
Hgdnfr	VCSYEEREKP	NCLNLQDSCK	TNYICRSRLA	DFFTNCQPES	RSVSSCLKEN
Hgrr2	SCSYEDKEKP	NCLDLRGVCR	TDHLCRSRLA	DFHANCRASY	QTVTSCPADN
Rgrr2	SCSYEDKEKP	NCLDLRSLCR	TDHLCRSRLA	DFHANCRASY	RTITSCPADN
Hgrr3	NCALPP.VAP	NCLELRRLCF	SDPLCRSRLV	DFQTHCHP..	MDILGTCATE
Rgrr3	SCALPS.VAP	NCLDLRSFCR	ADPLCRSRLM	DFQTHCHP..	MDILGTCATE

FIG.18G

```
          301                                                  350
Mgdnfr    YADCLLAYSG LIGTVMTPNY VDSS..SLSV APWCDCSNSG NDLEDCLKFL
Rgdnfr    YADCLLAYSG LIGTVMTPNY VDSS..SLSV APWCDCSNSG NDLEDCLKFL
Hgdnfr    YADCLLAYSG LIGTVMTPNY IDSS..SLSV APWCDCSNSG NDLEECLKFL
 Hgrr2    YQACLGSYAG MIGFDMTPNY VDSSPTGIVV SPWCSCRGSG NMEEECEKFL
 Rgrr2    YQACLGSYAG MIGFDMTPNY VDSNPTGIVV SPWCNCRGSG NMEEECEKFL
 Hgrr3    QSRCLRAYLG LIGTAMTPNF ASNVNTSVAL S..CTCRGSG NLQEECEMLE
 Rgrr3    QSRCLRAYLG LIGTAMTPNF ISKVNTTVAL G..CTCRGSG NLQDECEQLE
```

FIG.18H

```
        351                                                     400
Mgdnfr  NFFKDNTCLK NAIQAFGNGS DVTMWQPAP. PVQTTTATTT TAFRIKNKPS
Rgdnfr  NFFKDNTCLK NAIQAFGNGS DVTMWQPAP. PVQTTTATTT TAFRVKNKPL
Hgdnfr  NFFKDNTCLK NAIQAFGNGS DVTVWQPAF. PVQTTTATTT TALRVKNKPL
 Hgrr2  RDFTENPCLR NAIQAFGNGT NVNVSPKGP. SFQATQAPRV EKTPSLPDDL
 Rgrr2  RDFTENPCLR NAIQAFGNGT DVNMSPKGP. SLPATQAPRV EKTPSLPDDL
 Hgrr3  GFFSHNPCLT EAIAAKMRFH SQLFSQDWPH PTFAVMAHQN ENPAVRPQPW
 Rgrr3  KSFSQNPCLM EAIAAKMRFH RQLFSQDWAD STFSVMQQQN SSPALRPQLR
```

FIG.18I

```
          401                                                     450
Mgdnfr    GPACSENEIP THVLPPCANL QAQKLKSNVS GSTHLCLSDN DYGKDGLAGA
Rgdnfr    GPAGSENEIP THVLPPCANL QAQKLKSNVS GSTHLCLSDS DFGKDGLAGA
Hgdnfr    GPAGSENEIP THVLPPCANL QAQKLKSNVS GNTHLCISNG NYEKEGL.GA
 Hgrr2    SDSTS...LG TSVITTCTSV QEQGLKANNS KELSMCFTEL TTNIIPGSNK
 Rgrr2    SDSTS...LG TSVITTCTSI QEQGLKANNS KELSMCFTEL TTNISPGSKK
 Hgrr3    VPSLFSCTLP LILLLSLW~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
 Rgrr3    LPVLSFFILT LILLQTLW*~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
```

FIG.18J

```
        451                                         490
Mgdnfr  SSHITTKSMA APPSCGLSSL PVMVFTALAA LLSVSLAETS
Rgdnfr  SSHITTKSMA APPSCSLSSL PVLMLTALAA LLSVSLAETS
Hgdnfr  SSHITTKSMA APPSCGLSPL LVLVVTALST LLSLTETS~~
 Hgrr2  VIKPNSGPSR ARPSAALTVL SVLMLKLAL* ~~~~~~~~~~
 Rgrr2  VIKLNSGSSR ARLSAALTAL PLLMLTLAL* ~~~~~~~~~~
 Hgrr3  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
 Rgrr3  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
```

FIG.19A

GDNFR Family of Receptors

```
           1                                                   50
Consensus  MV..l...p .pp...m.l. llslalPl.. .lqgael.g. .Rl..dCv.A.
Hgdnfr                    MFLAT LYFALPLLDL LLSAEVSGGD RL..DCVKAS
Rgdnfr                    MFLAT LYFALPLLDL LMSAEVSGGD RL..DCVKAS
Hgrr2         MILANVF CLFFFLDDTL RSLASPSS.. LQGPELHGW. RPPVDCVRAN
Rgrr2             MLV FPSHYPDETL RSLASPSS.. LQGSELHGW. RPQVDCVRAN
Hgrr3      MVRPLNPRPL PPVVLMLLLL LPPS.PLP.L AAGDPLPTES RLMNSCLQAR
Rgrr3        MGLSRSPR PPPLVILLLV LSLWLPLG.. .TGNSLPTEN RLVNSCTQAR
```

FIG.19B

```
          51                                                  100
Consensus ..C.ae..Cs ..YrtLrqC. ag...nt.La sg.E...... C..A.e.L..
   Hgdnfr DQCLKEQSCS TKYRTLRQCV AGKETNFSLA SGLEAKDE.. CRSAMEALKQ
   Rgdnfr DQCLKEQSCS TKYRTLRQCV AGKETNFSLT SGLEAKDE.. CRSAMEALKQ
    Hgrr2 ELCAAESNCS SRYRTLRQCL AGRDRNTMLA NK.E...... CQAALEVLQE
    Rgrr2 ELCAAESNCS SRYRTLRQCL AGRDRNTMLA NK.E...... CQAALEVLQE
    Hgrr3 RKCQADPTCS AAYHHLDSCT ..SSISTPLP SE.EPSVPAD CLEAAQQLRN
    Rgrr3 KKCEANPACK AAYQHLDSCT ..PSLSSPLP SG.ESATSAA CLEAAQQLRN
```

FIG.19C

```
           101                                                  150
Consensus  ssLydCrCkR gMKke..CL. IYWs.h..l. .Gn..le.SP YEp.VtSrls
   Hgdnfr  KSLYNCRCKR GMKKEKNCLR IYWSMYQSLQ .GNDLLEDSP YEP.VNSRLS
   Rgdnfr  KSLYNCRCKR GMKKEKNCLR IYWSMYQSLQ .GNDLLEDSP YEP.VNSRLS
    Hgrr2  SPLYDCRCKR GMKKELQCLQ IYWSIHLGLT EGEEFYEASP YEP.VTSRLS
    Rgrr2  SPLYDCRCKR GMKKELQCLQ IYWSIHLGLT EGEEFYEASP YEP.VTSRLS
    Hgrr3  SSLIGCMCHR RMKNQVACLD IYWTVHRARS LGNYELDVSP YEDTVTSKPW
    Rgrr3  SSLIDCRCHR RMKHQATCLD IYWTVHPVRS LGDYELDVSP YEDTVTSKPW
```

FIG.19D

```
            151                                                200
Consensus   difr..s..s ....d..... ksn.CLdaAk aCnLnD.Ckk lRsaYi..C.
   Hgdnfr   DIFRVVPFIS DVFQQVEHIP KGNNCLDAAK ACNLDDICKK YRSAYITPCT
   Rgdnfr   DIFRAVPFIS DVFQQVEHIS KGNNCLDAAK ACNLDDTCKK YRSAYITPCT
    Hgrr2   DIFRLASIFS GTGADPVVSA KSNHCLDAAK ACNLNDNCKK LRSSYISICN
    Rgrr2   DIFRLASIFS GTGTDPAVST KSNHCLDAAK ACNLNDNCKK LRSSYISICN
    Hgrr3   KMNL..SKLN MLKPD..... .SDLCLKFAM LCTLNDKCDR LRKAYGEAC.
    Rgrr3   KMNL..SKLS MLKPD..... .SDLCLKFAM LCTLNDKCDR LRKAYGEAC.
```

FIG.19E

	201				250
Consensus	...S..erCn	RrkChkaLrq	FFdkvp..h.	ygmLfCsC..	.D.aC.ERRR
Hgdnfr	TSVS.NDVCN	RRKCHKALRQ	FFDKVPAKHS	YGMLFCSC..	RDIACTERRR
Rgdnfr	TSMS.NEVCN	RRKCHKALRQ	FFDKVPAKHS	YGMLFCSC..	RDIACTERRR
Hgrr2	REISPTERCN	RRKCHKALRQ	FFDRVPSEYT	YRMLFCSC..	QDQACAERRR
Rgrr2	REISPTERCN	RRKCHKALRQ	FFDRVPSEYT	YRMLFCSC..	QDQACAERRR
Hgrr3	...SG.PHCQ	RHVCLRQLLT	FFEKAAEPHA	QGLLLCPCAP	NDRGCGERRR
Rgrr3	...SG.IRCQ	RHLCLAQLRS	FFEKAAESHA	QGLLLCPCAP	EDAGCGERRR

FIG.19F

```
          251                                                      300
Consensus qTI.PsCsye ..ekPNCLdL r..Crtd.lC RSRLaDF.tn C....r.v.s
   Hgdnfr QTIVPVCSYE EREKPNCLNL QDSCKTNYIC RSRLADFFTN CQPESRSVSS
   Rgdnfr QTIVPVCSYE ERERPNCLSL QDSCKTNYIC RSRLADFFTN CQPESRSVSN
    Hgrr2 QTILPSCSYE DKEKPNCLDL RGVCRTDHLC RSRLADFHAN CRASYQTVTS
    Rgrr2 QTILPSCSYE DKEKPNCLDL RSLCRTDHLC RSRLADFHAN CRASYRTITS
    Hgrr3 NTIAPNC.AL PPVAPNCLEL RRLCFSDPLC RSRLVDFQTH C.HPMDILGT
    Rgrr3 NTIAPSC.AL PSVAPNCLDL RSFCRADPLC RSRLMDFQTH C.HPMDILGT
```

FIG.19G

```
          301                                                350
Consensus C.a.ny..CL .aY.GlIGt. MTPNyvdss. t...VapwC. CrgSGN..ee
   Hgdnfr CLKENYADCL LAYSGLIGTV MTPNYIDSSS ..LSVAPWCD CSNSGNDLEE
   Rgdnfr CLKENYADCL LAYSGLIGTV MTPNYVDSSS ..LSVAPWCD CSNSGNDLED
    Hgrr2 CPADNYQACL GSYAGMIGFD MTPNYVDSSP TGIVVSPWCS CRGSGNMEEE
    Rgrr2 CPADNYQACL GSYAGMIGFD MTPNYVDSNP TGIVVSPWCN CRGSGNMEEE
    Hgrr3 C.ATEQSRCL RAYLGLIGTA MTPNFASNVN TS..VALSCT CRGSGNLQEE
    Rgrr3 C.ATEQSRCL RAYLGLIGTA MTPNFISKVN TT..VALGCT CRGSGNLQDE
```

FIG.19H

```
           351                                                  400
Consensus  Cekfl.fF.. NpCL.nAIqA fgng...... .....p.fsv .....t.t.a
   Hgdnfr  CLKFLNFFKD NTCLKNAIQA FGNGS....D VTVWQPAFPV QTTTATTTTA
   Rgdnfr  CLKFLNFFKD NTCLKNAIQA FGNGS....D VTMWQPAPPV QTTTATTTTA
    Hgrr2  CEKFLRDFTE NPCLRNAIQA FGNGTNV... ......NVSP KGPSFQATQA
    Rgrr2  CEKFLRDFTE NPCLRNAIQA FGNGTDV... ......NMSP KGPSLPATQA
    Hgrr3  CEMLEGFFSH NPCLTEAIAA KMRFHSQLFS QDWPHPTFAV MAHQNENPAV
    Rgrr3  CEQLEKSFSQ NPCLMEAIAA KMRFHRQLFS QDWADSTFSV MQQQNSSPAL
```

FIG.19I

```
            401                                                450
Consensus   .rv...PsL. ...s....l. t.v...C..l Q.Q.LK.N.S .e...Cf.el
   Hgdnfr   LRVKNKP.LG PAGSENEIP. THVLPPCANL QAQKLKSNVS GNTHLCISNG
   Rgdnfr   FRVKNKP.LG PAGSENEIP. THVLPPCANL QAQKLKSNVS GSTHLCLSDS
    Hgrr2   PRVEKTPSLP DDLSDSTSLG TSVITTCTSV QEQGLKANNS KELSMCFTEL
    Rgrr2   PRVEKTPSLP DDLSDSTSLG TSVITTCTSI QEQGLKANNS KELSMCFTEL
    Hgrr3   RPQPWVPSLF SCTLPLILLL SLW
    Rgrr3   RPQLRLPVLS FFILTLILLQ TLW

            451                                               499
Consensus   ttn....sg. ...i...s.. A.pS.aL..L pvlmltala. LLS....S
   Hgdnfr   NYEKEGL.GA SSHITTKSMA APPSCGLSPL LVRVVTALST LLSLTETS
   Rgdnfr   DFGKDGLAGA SSHITTKSMA APPSCSLSSL PVLMLTALAA LLSVSLA
    Hgrr2   TTNIIPGSNK VIKPNSGPSR ARPSAALTVL SVLMLK.LAL
    Rgrr2   TTNISPGSKK VIKLNSGSSR ARLSAALTAL PLLMLTLAL
```

FIG.20A

```
Human GDNFRα              MFLATLYFALPLLDLLLSAEVSGGDRLDCVKASDQCLKE
Rat GDNFRα                MFLATLYFALPLLDLLMSAEVSGGDRLDCVKASDQCLKE
Human GRR2     MILANVFCLFFFLDDTLRSLASPSSLQGPELHGWRPPVDCVRANELCAAE
Rat GRR2            MLVFPSHYPDETLRSLASPSSLQGSELHGWRPCVDCVRANELCAAE

Human GDNFRα   QSCSTKYRTLRQCVAGKETNFSLASGLEAKDECRSAMEALKQKSLYNCRC
Rat GDNFRα     QSCSTKYRTLRQCVAGKETNFSLTSGLEAKDECRSAMEALKQKSLYNCRC
Human GRR2     SNCSSRYRTLRQCLAGRDRN.....TMLANKECQAALEVLQESPLYDCRC
Rat GRR2       SNCSSRYRTLRQCLAGRDRN.....TMLANKECQAALEVLQESPLYDCRC

Human GDNFRα   KRGMKKEKNCLRIYWSMYQSL.QGNDLLEDSPYEPVNSRLSDIFRVVPFI
Rat GDNFRα     KRGMKKEKNCLRIYWSMYQSL.QGNDLLEDSPYEPVNSRLSDIFRAVPFI
Human GRR2     KRGMKKELQCLQIYWSIHLGLTEGEEFYEASPYEPVTSRLSDIFRLASIF
Rat GRR2       KRGMKKELQCLQIYWSIHLGLTEGEEFYEASPYEPVTSRLSDIFRLASIF
```

FIG.20B

```
Human GDNFRα   SDVFQQVEHIPKGNNCLDAAKACNLDDICKKYRSAYITPCTTSVS.NDVC
Rat GDNFRα     SDVFQQVEHISKGNNCLDAAKACNLDDICKKYRSAYITPCTTSMS.NEVC
Human GRR2     SGTGADPVVSAKSNHCLDAAKACNLNDNCKKLRSSYISICNREISPTERC
Rat GRR2       SGTGTDPAVSTKSNHCLDAAKACNLNDNCKKLRSSYISICNREISPTERC

Human GDNFRα   NRRKCHKALRQFFDKVPAKHSYGMLFCSCRDIACTERRRQTIVPVCSYEE
Rat GDNFRα     NRRKCHKALRQFFDKVPAKHSYGMLFCSCRDIACTERRRQTIVPVCSYEE
Human GRR2     NRRKCHKALRQFFDRVPSEYTYRMLFCSCQDQACAERRRQTILPSCSYED
Rat GRR2       NRRKCHKALRQFFDRVPSEYTYRMLFCSCQDQACAERRRQTILPSCSYED

Human GDNFRα   REKPNCLNLQDSCKTNYICRSRLADFFTNCQPESRSVSSCLKENYADCLL
Rat GDNFRα     RERPNCLSLQDSCKTNYICRSRLADFFTNCQPESRSVSNCLKENYADCLL
Human GRR2     KEKPNCLDLRGVCRTDHLCRSRLADFHANCRASYQTVTSCPADNYQACLG
Rat GRR2       KEKPNCLDLRSLCRTDHLCRSRLADFHANCRASYRTITSCPADNYQACLG

Human GDNFRα   AYSGLIGTVMTPNYIDSS..SLSVAPWCDCSNSGNDLEECLKFLNFFKDN
Rat GDNFRα     AYSGLIGTVMTPNYVDSS..SLSVAPWCDCSNSGNDLEDCLKFLNFFKDN
Human GRR2     SYAGMIGFDMTPNYVDSSPTGIVVSPWCSCRGSGNMEEECEKFLRDFTEN
Rat GRR2       SYAGMIGFDMTPNYVDSNPTGIVVSPWCNCRGSGNMEEECEKFLRDFTEN
```

FIG.20C

```
Human GDNFRα   TCLKNAIQAFGNGSDVIVWQPAFPVQTTTATTTTALRVKNKPLGPAGSEN
Rat GDNFRα     TCLKNAIQAFGNGSDVIMWQPAPPVQTTTATTTTAFRVKNKPLGPAGSEN
Human GRR2     PCLRNAIQAFGNGTNVNVSPKGPSFQATCAPRVEKTPSLPDDLSDSTS..
Rat GRR2       PCLRNAIQAFGNGTDVNMSPKGPSLPATCAPRVEKTPSLPDDLSDSTS..

Human GDNFRα   EIPTHVLPPCANLQAQKLKSNVSGNTHLCISNGNYEKEGL.GASSHITTK
Rat GDNFRα     EIPTHVLPPCANLQAQKLKSNVSGSTHLCLSDSDFGKDGLAGASSHITTK
Human GRR2     .LGTSVITTCTSVQEQGLKANNSKELSMCFTELTTNIIPGSNKVIKPNSG
Rat GRR2       .LGTSVITTCTSIQEQGLKANNSKELSMCFTELTTNISPGSKKVIKLNSG

Human GDNFRα   SMAAPPSCGLSPLLVLVVT.ALSTLL..SLTETS
Rat GDNFRα     SMAAPPSCSLSSLPVLMLT.ALAALLSVSLAETS
Human GRR2     PSRARPSAALTVLSVLMLKLAL
Rat GRR2       SSRARLSAALTALPLLMLTLAL
```

FIG. 21A

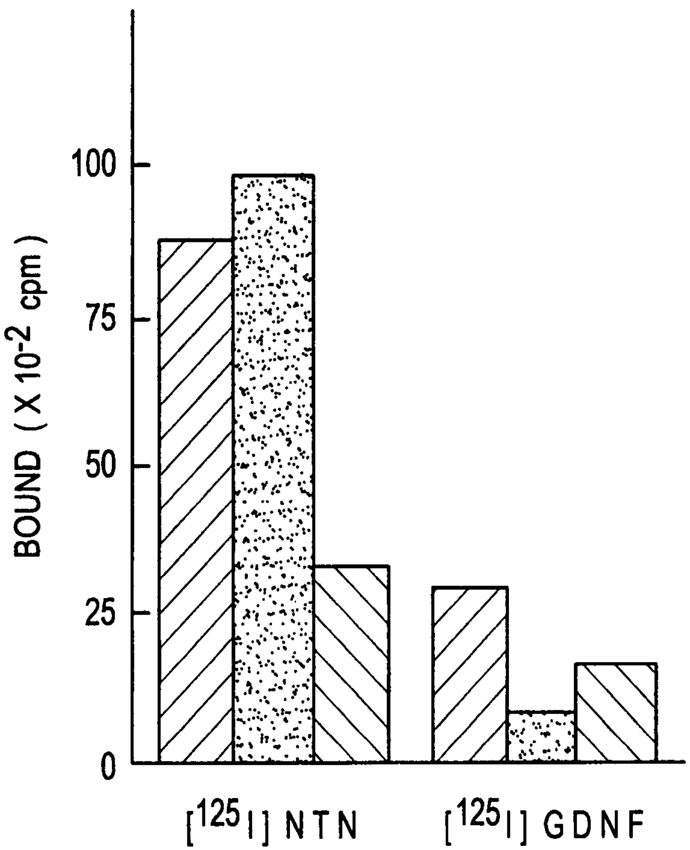


FIG. 21B

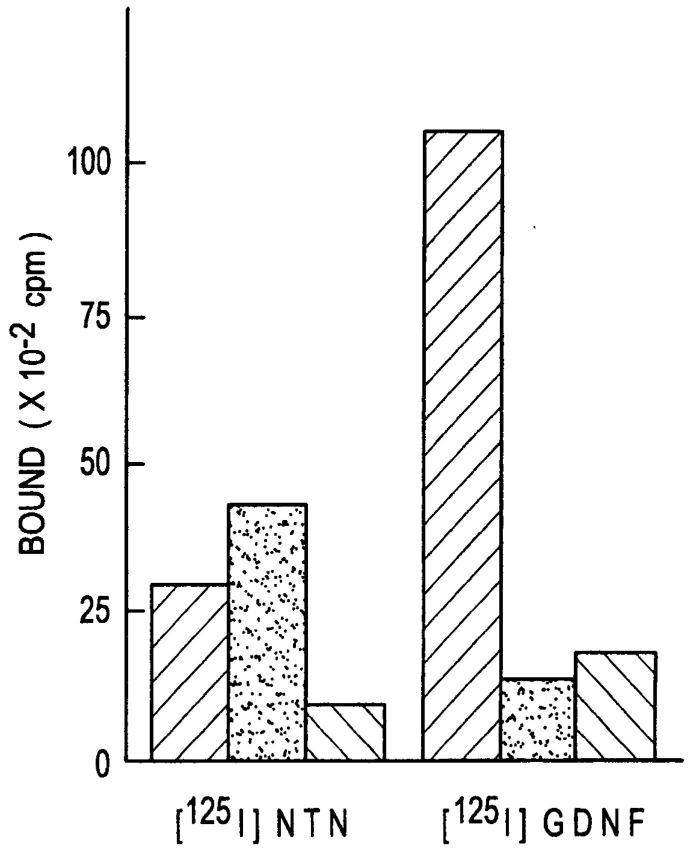


FIG.22

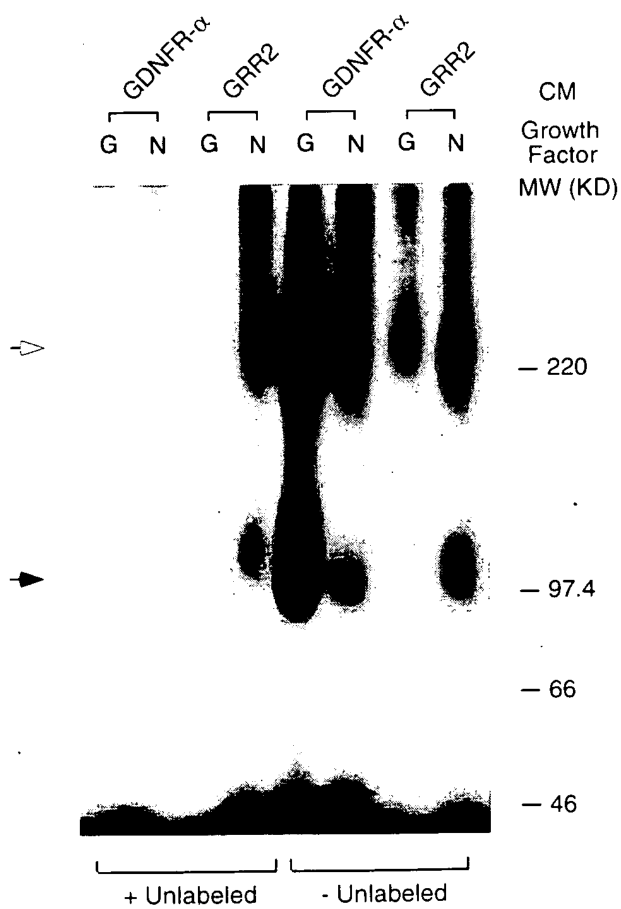

GDNFR-α
GRR2
GDNFR-α
GRR2
CM
G N G N G N G N
Growth Factor
MW (KD)
— 220
— 97.4
— 66
— 46
+ Unlabeled
- Unlabeled

FIG.23

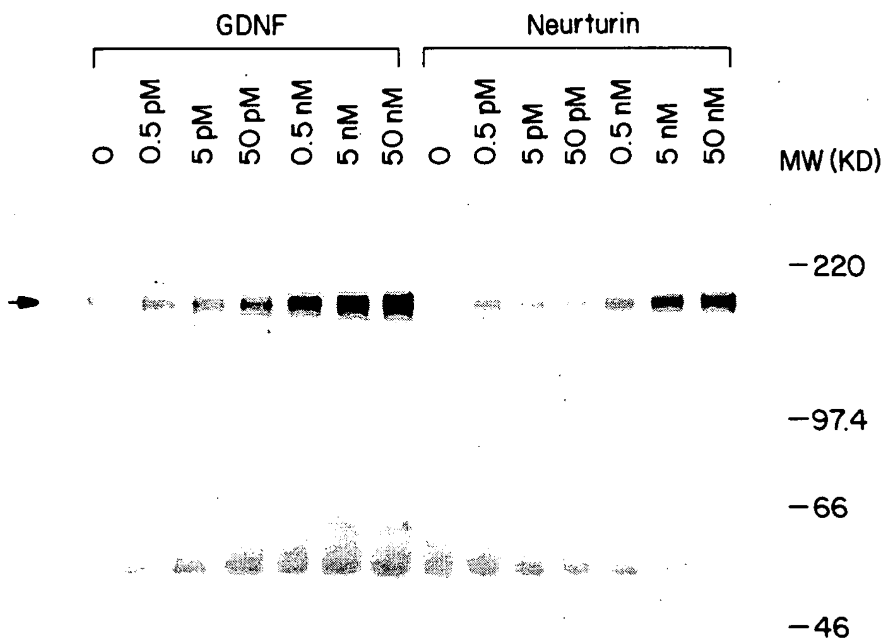

GDNF
Neurturin
0
0.5 pM
5 pM
50 pM
0.5 nM
5 nM
50 nM
0
0.5 pM
5 pM
50 pM
0.5 nM
5 nM
50 nM
MW (KD)
-220
-97.4
-66
-46

FIG.24

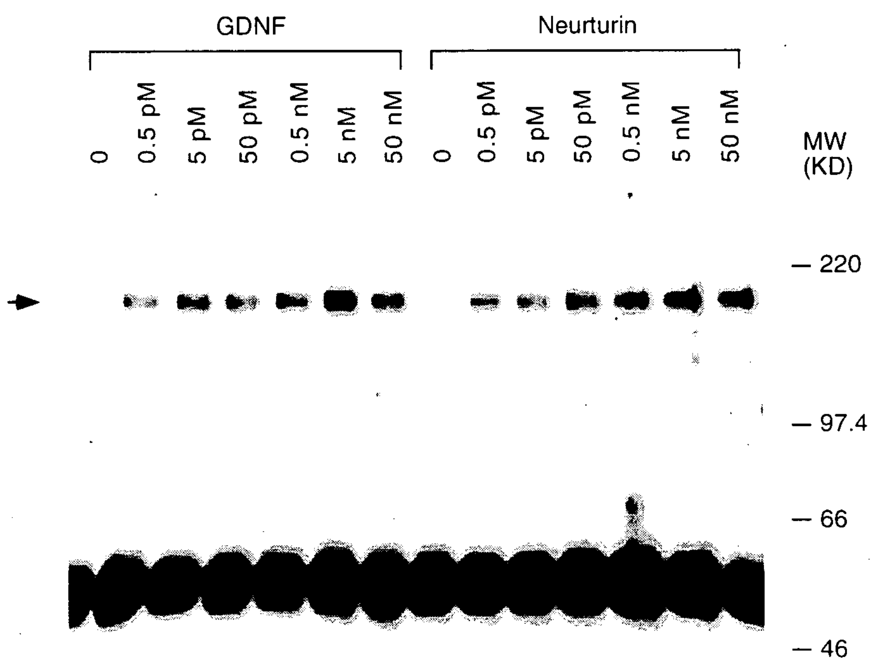

GDNF
Neurturin
0
0.5 pM
5 pM
50 pM
0.5 nM
5 nM
50 nM
0
0.5 pM
5 pM
50 pM
0.5 nM
5 nM
50 nM
MW
(KD)
— 220
— 97.4
— 66
— 46

FIG.25

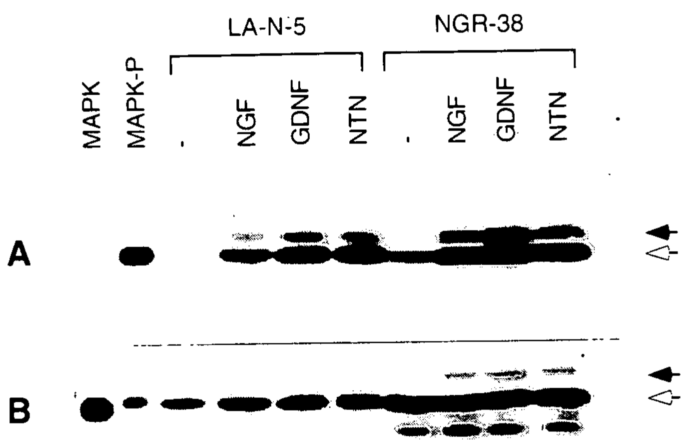


FIG.26A

```
           1                                                    50
CONSENSUS  .........P ....l.tl.s l..pl.l..S .....r...d Cv.A...C.a
    GDNFR  .......... ..MFLATLYF ALPLLDLLMS AEVSGGDRLD CVKASDQCLK
     GRR2  .....MLVFP SHYPDETLRS LASPSSLQGS ELHGWRPQVD CVRANELCAA
     GRR3  MGLSRSPRPP PLVILLLVLS LWLPLGTGNS LPTENRLVNS CTQARKKCEA

           51                                                  100
CONSENSUS  e..Cs..Yrt LrqC.ag... n........a ..eC..A.e. L..ssLydCR
    GDNFR  EQSCSTKYRT LRCCVAGKET NFSLTSGLEA KDECRSAMEA LKQKSLYNCR
     GRR2  ESNCSSRYRT LRCCLAGRDR N.....TMLA NKECQAALEV LQESPLYDCR
     GRR3  NPACKAAYQH LDSCTPSLSS PLPSGES.AT SAACLEAACQ LRNSSLIDCR

           101                                                 150
CONSENSUS  CkRgMKke.. CL.IYWs.h. .l..G...le .SPYE.pVtS rlsdifr..s
    GDNFR  CKRGMKKEKN CLRIYWSMYQ SL.QGNDLLE DSPYE.PVNS RLSDIFRAVP
     GRR2  CKRGMKKELQ CLQIYWSIHL GLTEGEEFYE ASPYE.PVTS RLSDIFRLAS
     GRR3  CHRRMKHQAT CLDIYWTVHP VRSLGDYELD VSPYEDTVTS ..KPWKMNLS
```

FIG.26.B

```
           151                                                   200
CONSENSUS  ..S....d.. ...ksn.CLd aAkaCnLnD. CkklRsaYi. .C....S..e
    GDNFR  FISDVFQQVE HISKGNNCLD AAKACNLDDT CKKYRSAYIT PCTTSMS.NE
     GRR2  IFSGTGTDPA VSTKSNHCLD AAKACNLNDN CKKLRSSYIS ICNREISPTE
     GRR3  KLSMLKPD.. ....SDLCLK FAMLCTLNDK CDRLRKAYGE AC....SG.I

           201                                                   250
CONSENSUS  rCnRrkChka LRqFFdkvp. .h.ygmLfCs C...D.aC.E RRRqTI.PsC
    GDNFR  VCNRRKCHKA LRQFFDKVPA KHSYGMLFCS C..RDIACTE RRRQTIVPVC
     GRR2  RCNRRKCHKA LRQFFDRVPS EYTYRMLFCS C..QDQACAE RRRQTILPSC
     GRR3  RCQRHLCLAQ LRSFFEKAAE SHAQGLLLCP CAPEDAGCGE RRRNTIAPSC

           251                                                   300
CONSENSUS  sve..e.PNC LdLrs.Crtd .lCRSRLaDF .tnC.p..r. .t.C.a.ny.
    GDNFR  SYEERERPNC LSLQDSCKTN YICRSRLADF FTNCQPESRS VSNCLKENYA
     GRR2  SYEDKEKPNC LDLRSLCRTD HLCRSRLADF HANCRASYRT ITSCPADNYQ
     GRR3  ALPSVA.PNC LDLRSFCRAD PLCRSRLMDF QTHCHPMDIL GT.C.ATEQS

           301                                                   350
CONSENSUS  .CL.aY.GlI Gt.MTPNyvd s..t...Vap wC.CrgSGN. .eeCekfl..
    GDNFR  DCLLAYSGLI GTVMTPNYVD SSSL..SVAP WCDCSNSGND LEDCLKFLNF
     GRR2  ACLGSYAGMI GFDMTPNYVD SNPTGIVVSP WCNCRGSGNM EEECEKFLRD
     GRR3  RCLRAYLGLI GTAMTPNFIS KVNTT..VAL GCTCRGSGNL QDECEQLEKS
```

FIG.26C

```
           351                                                400
CONSENSUS  F..NpCL.nA IqAfgng.dv .msq..p... .t.a...... rv...p.l..
    GDNFR  FKDNTCLKNA IQAFGNGSDV TMWQPAPPVQ TTTATTTTAF RVKNKP.LGP
     GRR2  FTENPCLRNA IQAFGNGTDV NMSPKGPSLP ATQAP..... RVEKTPSLPD
     GRR3  FSQNPCLMEA IAAKMRFHRQ LFSQDWADST FSVMCQQNSS PALRPQ....

           401                                                450
CONSENSUS  ..s......t .v...c...q .q.lk.n.s. ....c..... ..........
    GDNFR  AGS.ENEIPT HVLPPCANLQ AQKLKSNVSG STHLCLSDSD FGKDGLAGAS
     GRR2  DLSDSTSLGT SVITTCTSIQ EQGLKANNSK ELSMCFTELT TNISPGSKKV
     GRR3  .......... .......... .......... .......... ..........

           451                                     489
CONSENSUS  ......s..a ..s..l..LP vLmlt.l... l...l.ets
    GDNFR  SHITTKSMAA PPSCSLSSLP VLMLTALAAL LSVSLAETS
     GRR2  IKLNSGSSRA RLSAALTALP LLMLTLAL
     GRR3  .......... ......LRLP VLSFFILTLI LLOTLW
```